

Original Article

Computer-Aided Cervical Cancer Diagnosis Using Time-Lapsed Colposcopic Images

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Abstract: cervical cancer causes the fourth most cancer related deaths of women worldwide. Early detection of cervical intraepithelial neoplastic (cin) can significantly increase the survival rate of patients. In this paper, we propose a deep learning framework for the accurate identification of lsil+ (including cin and cervical cancer) using time-lapsed colposcopy images. The proposed framework involves two main components, i.e., key-frame feature encoding networks and feature fusion network. The features of the original (pre-acetic-acid) image and the colposcopy images captured at around 60s, 90s, 120s and 150s during the acetic acid test are encoded by the feature encoding networks. Several fusion approaches are compared, all of which outperform the existing automated cervical cancer diagnosis systems using a single time slot.

Keywords: Cervical Cancer Diagnosis, Colposcopy Imaging, Time-Lapsed Imaging, Computer-Aided Diagnosis (Cad), Medical Image Analysis, Machine Learning In Healthcare

INTRODUCTION

Prostate cancer leads to the fourth highest number of deaths in male cancers, carrying high risks of morbidity and mortality. Nevertheless, the prostate cancer is slow growing, so its progression through precancerous changes provides opportunities for prevention, early detection, and treatment. The main challenge of prostate cancer elimination centres on the low- and middle-income countries (LMICs) where gender discrimination and extreme poverty severely limit a woman's choice to seek care – resulting in over 88% of deaths from Prostate cancer. Image processing is a method to convert an image into digital form and perform some operations on it, in order to get an enhanced image or to extract some useful information from it. It is a type of signal dispensation in which input is image, like video frame or photograph and output may be image or characteristics associated with that image. Usually Image Processing system includes treating images as two dimensional signals while applying already set signal processing methods to them. It is among rapidly growing technologies today, with its applications in various aspects of a business. Image Processing forms core research area within engineering and computer science disciplines.

1.1 IMAGE PROCESSING BASICALLY INCLUDES THE FOLLOWING THREE STEPS.

- Importing the image with optical scanner or by digital photography.
- Analysing and manipulating the image which includes data compression and image enhancement and spotting patterns that are not to human eyes like satellite photographs.
- Output is the last stage in which result can be altered image or report that is based on image analysis.

1.2 PURPOSE OF IMAGE PROCESSING:

The purpose of image processing is divided into 5 groups. They are:

1. Visualization - Observe the objects that are not visible.
2. Image sharpening and restoration - To create a better image.
3. Image sharpening and restoration - To create a better image.
4. Measurement of pattern – Measures various objects in an image.
5. Image Recognition – Distinguish the objects in an image.

1.3 TYPES:

The two types of methods used for Image Processing are analog and digital Image Processing. Analog or visual techniques of image processing can be used for the hard copies like printouts and photographs. Image analysts use various fundamentals of interpretation while using these visual techniques. The image processing is not just confined to area that has to be studied but on knowledge of analyst. Association is another important



tool in image processing through visual techniques. So analysts apply a combination of personal knowledge and collateral data to image processing.

Digital Processing techniques help in manipulation of the digital images by using computers. As raw data from imaging sensors from satellite platform contains deficiencies. To get over such flaws and to get originality of information, it has to undergo various phases of processing. The three general phases that all types of data have to undergo while using digital technique are Pre- processing, enhancement and display, information extraction.

APPLICATION:

- Intelligent Transportation Systems – This technique can be used in Automatic number plate recognition and Traffic sign recognition.
- Remote Sensing – For this application, sensors capture the pictures of the earth’s surface in remote sensing satellites or multi – spectral scanner which is mounted on an aircraft. These pictures are processed by transmitting it to the Earth station. Techniques used to interpret the objects and regions are used in flood control, city planning, resource mobilization, agricultural production monitoring, etc.
- Moving object tracking – This application enables to measure motion parameters and acquire visual record of the moving object. The different types of approach to track an object are:
 - Motion based tracking
 - Recognition based tracking
- Defence surveillance – Aerial surveillance methods are used to continuously keep an eye on the land and oceans. This application is also used to locate the types and formation of naval vessels of the ocean surface. The important duty is to divide the various objects present in the water body part of the image. The different parameters such as length, breadth, area, perimeter, compactness are set up to classify each of divided objects. It is important to recognize the distribution of these objects in different directions that are east, west, north, south, northeast, northwest, southeast and south west to explain all possible formations of the vessels. We can interpret the entire oceanic scenario from the spatial distribution of these objects.
- Biomedical Imaging techniques – For medical diagnosis, different types of imaging tools such as X- ray, Ultrasound, computer aided tomography (CT) etc. are used. The diagrams of X- ray, MRI, and computer aided tomography (CT) are given below.
- Some of the applications of Biomedical imaging applications are as follows:
 - Heart disease identification– The important diagnostic features such as size of the heart and its shape are required to know in order to classify the heart diseases. To improve the diagnosis of heart diseases, image analysis techniques are employed to radiographic images.
 - Lung disease identification – In X- rays, the regions that appear dark contain air while region that appears lighter are solid tissues. Bones are more radio opaque than tissues. The ribs, the heart, thoracic spine, and the diaphragm that separates the chest cavity from the abdominal cavity are clearly seen on the X-ray film.
 - Digital mammograms – This is used to detect the breast tumour. Mammograms can be analysed using Image processing techniques such as segmentation, shape analysis, contrast enhancement, feature extraction, etc.
 - Automatic Visual Inspection System – This application improves the quality and productivity of the product in the industries.

A wide research is being done in the Image processing technique.

1. Cancer Imaging – Different tools such as PET, MRI, and Computer aided Detection helps to diagnose and be aware of the tumour.
2. Brain Imaging – Focuses on the normal and abnormal development of brain, brain ageing and common disease states.
3. Image processing – This research incorporates structural and functional MRI in neurology, analysis of bone shape and structure, development of functional imaging tools in oncology, and PET image processing software development.
4. Imaging Technology – Development in image technology have formed the requirement to establish whether new technologies are effective and cost beneficial. This technology works under the following areas:
 - Magnetic resonance imaging of the knee
 - Computer aided detection in mammography

- Endoscopic ultrasound in staging the esophageal cancer
- Magnetic resonance imaging in low back pain

Ophthalmic Imaging – This works under two categories:

1. Development of automated software- Analyses the retinal images to show early sign of diabetic retinopathy.
2. Development of instrumentation – Concentrates on development of scanning laser ophthalmoscope.

We all are in midst of revolution ignited by fast development in computer technology and imaging. Against common belief, computers are not able to match humans in calculation related to image processing and analysis. But with increasing sophistication and power of the modern computing, computation will go beyond conventional, Von Neumann sequential architecture and would contemplate the optical execution too. Parallel and distributed computing paradigms are anticipated to improve responses for the image processing results.

1.4 BIOMEDICAL IMAGE PROCESSING

Biomedical imaging concentrates on the capture of images for both diagnostic and therapeutic purposes. Snapshots of in vivo physiology and physiological processes can be garnered through advanced sensors and computer technology. Biomedical imaging technologies utilize either x-rays (CT scans), sound (ultrasound), magnetism (MRI), radioactive pharmaceuticals (nuclear medicine: SPECT, PET) or light (endoscopy, OCT) to assess the current condition of an organ or tissue and can monitor a patient over time over time for diagnostic and treatment evaluation.

The science and engineering behind the sensors, instrumentation and software used to obtain biomedical imaging has been evolving continuously since the x-ray was first invented in 1895. Modern x-rays using solid-state electronics require just milliseconds of exposure time, drastically reducing the x-ray dose originally needed for recording to film cassettes. The image quality has also improved, with enhanced resolution and contrast detail providing more reliable and accurate diagnoses.

The limitations of what x-rays could reveal were partially addressed through the introduction of contrast medium to help visualize organs and blood vessels. First introduced as early as 1906, contrast agents, too, have evolved over the years. Today, digital x-rays enable images to more easily be shared and compared.

Digital imaging gave rise to the CT scanner and allows physicians to watch real-time x-rays on a monitor – a technique known as x-ray fluoroscopy – to help guide invasive procedures such as angiograms and biopsies. No longer limited to simple anatomical imaging, current research is focusing on what can be gleaned through functional imaging. Biomedical engineers are using CT and MRI to measure the blood perfusion of tissue; especially important after a heart attack or suspected heart attack. Researchers are also using functional MRI (fMRI) to measure different types of brain activity following strokes and traumatic head injuries.

PET scans – which use a radioactive tracer PET to measure metabolic changes, blood flow and oxygen use – have also improved with technological advancements. PET scans enable researchers to compare, for example, brain activity during periods of depression based on the chemical activity in the brain.

Optical molecular imaging technologies represent a new area of research that can be used to image human cells and molecules without the need for a biopsy or cell culture. Using contrast or imaging agents that attach to specific molecules, disease processes, such as cancer, can be spotted before they render their effects at the level of gross pathology.

Bio-medical image analysis is an interdisciplinary field which includes: biology, physics, medicine and engineering. It deals with application of image processing techniques to biological or medical problems. Medical images to be analyzed contain a lot of information regarding the anatomical structure under investigation to reveal valid diagnosis and thereby helping doctors to choose adequate therapy. Doctors usually analyze these medical images manually through visual interpretation. But visual analysis of these images by human observers is limited due to variation in interpersonal interpretations, fatigue errors, surrounding disturbances and moreover this kind of analysis is purely subjective. On the other hand, automated analysis of these images using computers with suitable techniques favours the objective analysis by an expert and thereby improving the diagnostic confidence and accuracy of analysis. This survey is a consolidation of the exhaustive literature records related to biomedical image analysis.

BIOMEDICAL IMAGE PREPROCESSING:

Pre-processing is a common name for operations with images at the lowest level of abstraction both input and output are intensity of biomedical images. These iconic biomedical images are of the same kind as the original data captured by the sensor, with an intensity of biomedical image usually represented by a matrix of image function values (brightness's).

The aim of pre-processing is an improvement of the image data that suppresses unwilling distortions or enhances some image features important for further processing, although geometric transformations of images (e.g. rotation, scaling, and translation) are classified among pre-processing methods here since similar techniques are used.

Image processing methods have opened the opportunity to extract quantitative information from confocal microscopy images of biological samples, dramatically increasing the range of questions that can be addressed experimentally in biology. Biologists aim to understand how cells behave and what genes do to build a normal animal, and what goes wrong in disease or upon injury. For this, they look at how alterations in gene function and application of drugs affect tissue, organ or whole body integrity, using confocal microscopy images of samples stained with cell specific markers. Image-processing methods have enormous potential to extract information from this kind of samples, but surprisingly, they are still relatively underexploited. One useful parameter to quantify is cell number. Cell number is the balance between cell division and cell death; it is controlled tightly during growth and it can be altered in disease, most notoriously neuro degeneration and cancer. Injury (e.g. spinal cord injury) results in an increase in cell death, plus a homeostatic regulation of cell proliferation.

Thus to understand normal animal development, injury responses and disease, it is important to find out how many cells die or divide, or how many cells of a given type there are in an organ. Generally, cells are counted using automated methods after dissociating cells from a tissue (e.g. fluorescence-activated cell sorting, FACS, based), or when they are distributed in a dish in cell culture experiments, using image processing techniques in 2D. However, these approaches alter the normal cellular contexts and the procedures themselves can alter the relative numbers of cells. To maintain information relevant to how genes and cells behave in the organism, it is best to count cells in vivo (i.e. in the intact animal) or at least in an entire organ or tissue (i.e. in situ). Counting in vivo or in situ is generally carried out manually, or it consists of estimates of number of cells stained with a particular cell marker or inferences from anatomical alterations. These methods can be extremely time-consuming, estimates can be inaccurate, and the questions that can be addressed using these methods are limited. Manual counting can be experimentally cumbersome, tedious, labour intensive and error prone. The advent of confocal microscopy, which allows the capture of 3D images, has enabled the development of automatic and semi-automatic image processing methods to count cells in whole tissues or entire small animals.

APPLICATION:

It includes the analysis, enhancement and display of images captured via x-ray, ultrasound, MRI, nuclear medicine and optical imaging technologies. Image reconstruction and modelling techniques allow instant processing of 2D signals to create 3D images.

1.5 CELL SEGMENTATION

The identified background label, along with the *segmented* nuclei, is used in the seeded machine learning *segmentation* of the *cell* marker image. This approach allows for the identification and separation of *cells*. For each nucleus, the approach will identify a corresponding *cell*. Automatic and reliable characterization of cells in cell cultures is key to several applications such as cancer research and drug discovery. Given the recent advances in light microscopy and the need for accurate and high-throughput analysis of cells, automated algorithms have been developed for segmenting and analyzing the cells in microscopy images. Nevertheless, accurate, generic and robust whole-cell segmentation is still a persisting need to precisely quantify its morphological properties, phenotypes and sub-cellular dynamics.

Automatic cell segmentation and dead cell detection in microscopic images play a very important role in the study of the behaviour of lymphocytes. A new *cell segmentation* algorithm using split and merge techniques were proposed a new method for *cell segmentation* in fluorescence *microscopy* images.

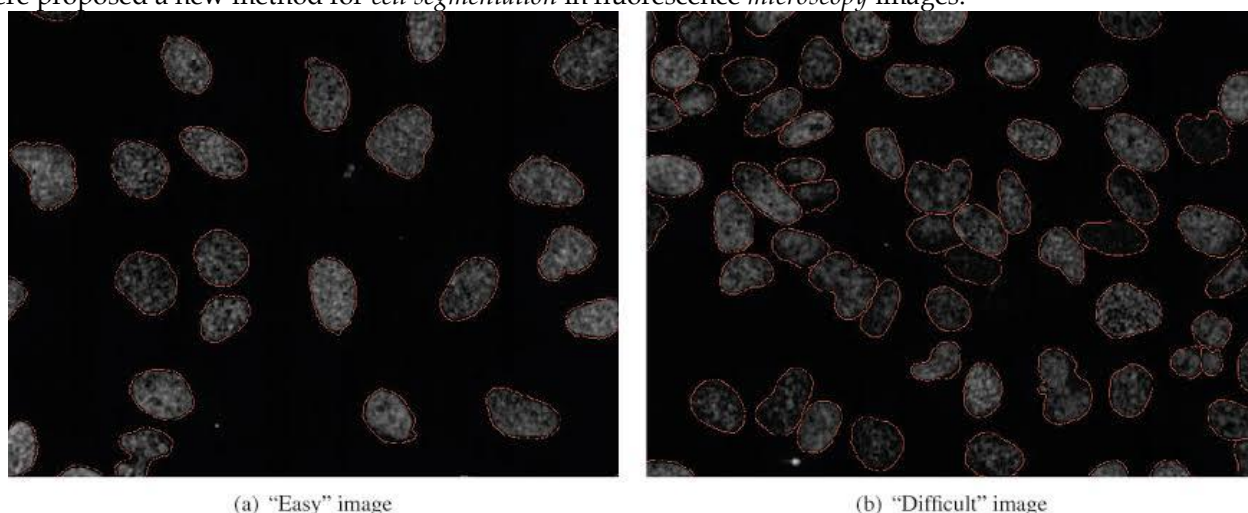


Figure 1 cell Segmentation

The cell segmentation has very high practical significance in medical diagnosis. But the cell image has the problems of accretive cells, incoherent cell boundary, and the internal cavity that make it difficult to image segmentation.

In this cell segmentation a machine learning algorithm based on distance transform is proposed to solve images of cells adhesion. Firstly, image enhancement is carried out as the image pre-processing, then the OTSU threshold segmentation is used to rough segment the image, finally the machine learning algorithm by optimizing the seed points is adopt for fine segmentation. Therefore, the machine learning segmentation based on distance transformation transform is practical according to the accretive cell images.

Reliable cell segmentation plays an important role in biological imaging studies, though continues to be challenging due to the complex nature of many imaging scenes. The approach here uses a novel immersion simulation based self-organizing (ISSO) transform, an automated method for image segmentation. The method allows users to customize the immersion simulation process via user-defined or default self-organizing functions to incorporate prior information into segmentation.

A Size Filter based on the ISSO transform is implemented and applied to various images and benchmark microscopy datasets from recent studies. With benchmark error rates well below those reported results in the literature, the comparison with other algorithms clearly demonstrates the benefits and flexibility of the ISSO method on various types of images.

CELL COUNTING

Cell counting is any of various methods for the *counting* or similar quantification of *cells* in the life sciences, including medical diagnosis and treatment. It is an important subset of cytometry, with applications in research and clinical practice.

For over 100 years the hemocytometer has been used by cell biologists to count cells. It was first developed for the quantization of blood cells but became a popular and effective tool for counting a variety of other cell types, particles, and even small organisms.

Cell counting is any of various methods for the *counting* or similar quantification of *cells* in the life sciences, including *medical* diagnosis and treatment. It is an important subset of cytometry, *with* applications in research and clinical practice. For example, the complete blood count can help a physician to determine why a patient feels unwell and what to do to help. Cell counts within liquid media (such as blood, plasma, lymph, or laboratory reinstate) are usually expressed as a number of cells per unit of volume, thus expressing a concentration (for example, 5,000 cells per millilitre).

For microbiology, cell culture and many of the applications that require use of cell suspensions, it is necessary to determine the concentration of cells. The device used for determining the number of cells per unit volume of a suspension is called a counting chamber.

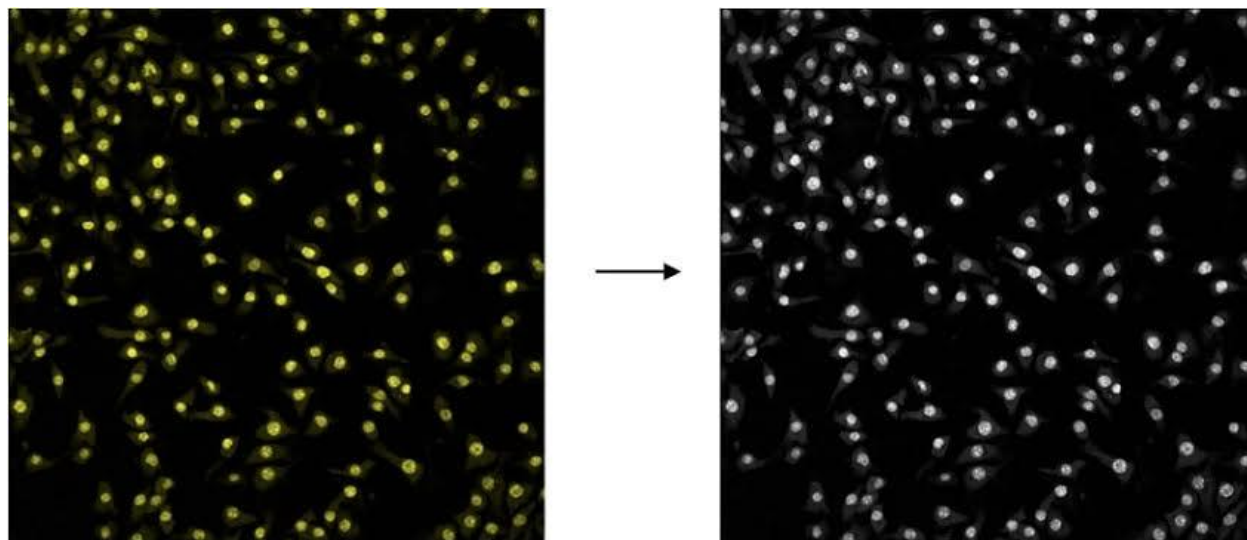


Figure 2 Cell Counting

LITERATURE REVIEW

2.1 A REVIEW FOR PROSTRATE HISTOPATHOLOGY IMAGE ANALYSIS USING MACHINE VISION APPROACHES

Chen Li, Hao Che et.al., has proposed. In this paper prostrate histopathology image analysis plays a very importation role in the cancer diagnosis and medical treatment processes, since the 1980s, more and more effective machine vision techniques are introduced and applied in this field to assist histopathologists to obtain a more rapid, stable, objective, and quantified analysis result. To discover the inner relation between the visible images and the actual diseases, a variety of machine vision techniques are used to help the histopathologists to get to know more properties and characteristics of prostrate tissues, referring to artificial intelligence, pattern recognition, and machine learning algorithms. Furthermore, because the machine vision approaches are usually semi- or full-automatic computer based methods, they are very efficient and labour cost saving, supporting a technical feasibility for prostrate histopathology study in our current big data age. Hence, in this article, we comprehensively review the development history of this research field with two crossed pipelines, referring to all related works since 1988 till 2020. In the first pipeline, all related works are grouped by their corresponding application goals, including image segmentation, feature extraction, and classification. By this pipeline, it is easy for histopathologists to have an insight into each special application domain and find their interested applied machine vision techniques. In the second pipeline, the related works on each application goals are reviewed by their detailed technique categories. Using this pipeline, machine vision scientists can see the dynamic of technological development clearly and keep up with the future development trend in this interdisciplinary field.

In the future, machine vision and pathological imaging techniques should not be developed mutually independent, but should be further integrated into an organic whole with the functions of real-time pathological image analysis under the microscopy or end microscopy (e.g., virtual staining and class labelling of pathological images). Specifically, the programs or software for image analysis of pathological images will be integrated into microscopes with small-sized high-performance computing chips. In this way, pathologists will be more easy to observe cells or tissue types in the current field of view, and judge their normal or abnormal probability through the lens in real time. In addition, they will be able to observe in the lens various virtual stained images obtained with basic staining. At the same time, the corresponding data analysis report and virtual staining image will be sent to the mobile phone, computer or mailbox according to the settings.

2.2 A SURVEY FOR PROSTATE CYTOPATHOLOGY IMAGE ANALYSIS USING DEEP LEARNING

MdMamunurRahaman, Chen Let.al, has proposed. In this paper Prostrate cancer is one of the most common and deadliest cancers among men . Despite that, this cancer is entirely treatable if it is detected at a precancerous stage. Pap smear test is the most extensively performed screening method for early detection of prostrate cancer. However, this hand-operated screening approach suffers from a high false-positive result because of human errors. To improve the accuracy and manual screening practice, computer-aided diagnosis methods based on deep learning is developed widely to segment and classify the prostrate cytology images automatically. In this survey, we provide a comprehensive study of the state of the art approaches based on deep learning for the analysis of prostrate cytology images. Firstly, we introduce deep learning and its simplified architectures that have been used in this field. Secondly, we discuss the publicly available prostrate cytopathology datasets and evaluation metrics for segmentation and classification tasks. Then, a thorough review of the recent development of deep learning for the segmentation and classification of prostrate cytology images is presented. Finally, we investigate the existing methodology along with the most suitable techniques for the analysis of pap smear cells.

In this paper, we examined studies related to prostrate cytopathology image segmentation and classification based on deep learning techniques. Besides, major deep learning concepts and their popular architectures are also explained. The review showed that prostrate cytopathology image analysis in deep learning is an increasing topic of interest. Most of the state-of-the-art methods that have been proposed for the segmentation and classification are applied to the same dataset. Thus, it is obvious to distinguish which algorithm is better than others. The Herlev dataset and ISBI challenge dataset are the publicly available benchmark datasets. MS-CNN, along with shape prior based method and MASK-RCNN merged with LFCCRF give superior performance for the segmentation of overlapping and non overlapping prostrate cell respectively. For the classification work, the combination of CNN(AlexNet) along with transfer learning and decision tree-based algorithm has better recognition ability. So, it is observed that compound algorithms can improve the performance of a classifier. AlexNet, VGGNet, and ResNet are found to be the most popular CNN architecture for feature extraction in this field. It is perceived that CNN has achieved outstanding performance in the task of segmentation and classification, which will help the patient for the early detection, diagnosis, and treatment of prostrate cancer. However, there is still room for improvement. First of all, texture feature is a significant low level feature that can describe the content or region of an image very adequately. Hence, concatenation of some novel texture descriptors such as hybrid colour local binary patterns (HCLBP) , moment invariant features, wavelet features, local binary pattern (LBP) [176] and elongated quandary pattern (EQP) with deep features can lead to a superior performance of network model. Secondly, researchers can develop entirely new CNN architecture for the analysis of prostrate pap smear cells. Thirdly, the analysis of overlapping cells is still a big challenge. Fourthly, designing an algorithm that can analyse whole slide images, which may contain millions of cells, is still an open challenge. Fifthly, to the best of our knowledge, there are only three open sources pap smear database is available with a significantly imbalanced ratio of positive and negative, so to create a public dataset will be beneficial for future researchers. Finally, attempts have been made to create deep learning enhanced mobile phone microscopy . So to develop a mobile phone application that can use the mobile phone microscopy to automatically analyse pap slides would be extremely useful.

2.3 AN APPLICATION OF TRANSFER LEARNING AND ENSEMBLE LEARNING TECHNIQUES FOR PROSTATE HISTOPATHOLOGY IMAGE CLASSIFICATION

Dan Xue ,Xiaomin Zhou et.al, has proposed. In this paper In recent years, researches are concentrating on the effectiveness of Transfer Learning (TL) and Ensemble Learning (EL) techniques in prostrate histopathology image analysis. However, there have been very few investigations that have described the stages of differentiation of prostrate histopathological images. Therefore, in this article, we propose an Ensemble Transfer Learning (ETL) framework to classify well, moderate and poorly differentiated prostrate histopathological images. First of all, we have developed Inception-V3, Xception, VGG-16, and Resnet-50 based TL structures. Then, to enhance the classification performance, a weighted voting based EL strategy is introduced. After that, to evaluate the proposed algorithm, a dataset consisting of 307 images, stained by three immunohistochemistry methods (AQP, HIF, and VEGF) is considered. In the experiment, we obtain the highest overall accuracy of 97.03% and 98.61% on AQP staining images and poor differentiation of VEGF staining images, individually. Finally, an additional experiment for classifying the benign cells from the malignant ones is carried out on the Herlev dataset and obtains an overall accuracy of 98.37%.

In this paper, weighted voting based EL is proposed to classify prostrate histopathological images. Especially, three prostrate cancer differentiation stages are classified, where the highest overall accuracy of 97.03% is achieved on AQP staining method. Meanwhile, the highest accuracy of 98.61% is achieved on poorly differentiated of VEGF staining. However, this method presents some deficiencies worthy to be pointed out. Firstly, we use four base learners, it requires a very sophisticated computer for its implementation and presents very high computational cost, and it adds to the workload as well. Secondly, there is no patient-level label for our current IHC dataset, so this paper does not do basic studies based on patients. At the moment, we are collecting more data and working in this direction. In the future, we plan to develop more efficient and simple systems to do the classification of prostrate histopathology images.

2.4 PROSTRATE HISTOPATHOLOGY IMAGE CLASSIFICATION USING MULTILAYER HIDDEN CONDITIONAL RANDOM FIELDS AND WEAKLY SUPERVISED LEARNING

C. Li¹, H. Chen¹, et al., has proposed. In this paper a novel Multilayer Hidden Conditional Random Fields (MHCRFs) based Prostrate Histopathology Image Classification (CHIC) model is proposed to classify well, moderate and poorly differentiation stages of prostrate cancer using a Weakly Supervised Learning strategy. First, colour, texture and Deep Learning features are extracted to represent the histopathological image patches. Then, based on the extracted features, Artificial Neural Network, Support Vector Machine and Random Forest classifiers are designed to calculate the patch-level classification probabilities. Thirdly, effective classifiers are selected to generate unary and binary potentials. Lastly, using the generated potentials, the final image level classification results are predicted by our MHCRF model, and an overall accuracy around 77.32% is obtained on six practical prostrate histopathological image datasets with more than 600 immuno histochemical (IHC) stained samples. Among the six test accuracies, the highest reaches 88%. Furthermore, we also test our MHCRF method with a gastric hematoxylin-eosin (HE) stained histopathological image dataset including 200 images for an extended experiment, and achieve an accuracy of 93%.

In this paper, we propose a weakly supervised MHCRF model to classify the prostrate histopathological images into well, moderate and poorly differentiation stages. The proposed MHCRF method not only considers the classical color and texture features, but also combines the state-of-the-art deep learning techniques into the framework. Furthermore, this MHCRF model build both unary and binary potentials to describe the spatial relationship between the image locations. In the experiment, the proposed method is tested on the six prostrate IHC datasets and obtains an around overall classification accuracy of 77.32% and the highest one of the six is 88%, showing the effectiveness and potential of the method. In addition, we carry out extended experiments on a gastric HE dataset, achieving overall accuracy of 93%, which can fully demonstrate the generalization ability of our MHCRF model.

2.5 ENSEMBLE LEARNERS OF MULTIPLE DEEP CNNs FOR PULMONARY NODULES CLASSIFICATION USING CT IMAGES

Baihua Zhang, Shouliang Qiet, et al., has proposed. In this paper Various deep convolutional neural networks (CNNs) have been used to distinguish between benign and malignant pulmonary nodules using CT images. However, single learner usually presents unsatisfied performance due to limited hypothesis space, or falling into local minima, or wrong selection of hypothesis space. To tackle these issues, we propose to build ensemble learners through fusing multiple deep CNN learners for pulmonary nodules classification. CT image patches of 743 nodules are extracted from LIDC-IDRI database and utilized. First, eight deep CNN learners with different architectures are trained and evaluated by 10-fold cross-validation. Each nodule has eight predictions from the eight primary learners. Second, we fuse these eight predictions by the strategies of majority voting (VOT), averaging (AVE), or machine learning. Specifically, different machine learning algorithms including K-NearestNeighbor (KNN), Support Vector Machines (SVM), Naive Bayes (NB), Decision Trees (DT), Multi-layer Perceptron (MLP), Random Forests (RF), Gradient Boosting Regression Trees (GBRT) and Adaptive Boosting (AdaBoost) are implemented. Moreover, the correlation coefficients between the predictions of 10 ensemble learners are calculated, and the hierarchical clustering dendrogram is drawn. It is found that the ensemble learners achieve higher prediction accuracy (84.0% vs 81.7%) than single CNN learner. The overlap ratio among the 10 ensemble learners is much higher than that of the 8 primary learners (62.9% vs 33.2%). In addition, it is shown that ensemble learners are roughly divided into three categories: the first (SVM, MLP, GBRT and RF) achieves the best performance; the second (VOT and AVE) is better than the third (AdaBoost, DT, NB and KNN). VOT and AVE yield higher recall than the machine learning algorithms. These results indicate that ensemble learners based on multiple CNN learners can achieve better performances for

pulmonary nodules classification using CT images and that preferred fusion strategies include SVM, MLP, GBRT and RF.

Deep CNN models with different network architectures can be constructed to classify pulmonary nodule in CT images and these models result in moderate or good performance. The ensemble learners resulted from fusing the predictions of multiple CNNs can achieve better classification performance than single CNN model. The fusion strategy can be VOT, AVE and machine learning algorithms. Correctly selecting algorithms of SVM, MLP, GBRT and RF will lead to higher ACC and lower recall than VOT and AVE. Overall, the proposed framework is a step forward for the ensemble learning, providing with competitive performance for pulmonary nodule classification. Our study can be extended to other classification tasks in medical images

2.6 CONSIDERATIONS FOR A PAP SMEAR IMAGE ANALYSIS SYSTEM WITH CNN FEATURES

SrishtiGautam, Harinarayan K. K., NirmalJith, et.al, has proposed. In this paper It has been shown that for automated PAP-smear image classification, nucleus features can be very informative. Therefore, the primary step for automated screening can be cell-nuclei detection followed by segmentation of nuclei in the resulting single cell PAP-smear images. We propose a patch based approach using CNN for segmentation of nuclei in single cell images. We then pose the question of ion of segmentation for classification using representation learning with CNN, and whether low-level CNN features may be useful for classification. We suggest a CNN-based feature level analysis and a transfer learning based approach for classification using both segmented as well full single cell images. We also propose a decision-tree based approach for classification. Experimental results demonstrate the effectiveness of the proposed algorithms individually (with low level CNN features), and simultaneously proving the sufficiency of cell-nuclei detection (rather than accurate segmentation) for classification. Thus, we propose a system for analysis of multi cell PAP-smear images consisting of a simple nuclei detection algorithm followed by classification using transfer learning.

In this paper, we reported a PAP-smear image analysis system for prostate cancer screening for both single and multi cell images. The image analysis generally consists of three steps: detection, segmentation and classification. We propose a simple nuclei detection algorithm for multi-cell images, and a patch-based CNN approach with selective pre-processing for segmentation. This approach results in an overall F-score of 0.90 on Herlev dataset. For classification, we propose feature level analysis using transfer learning on Alexnet on both single and multi-cell images. A decision-tree based classification is proposed as an alternative to the multi-class classification. Further, we prove through experimentation that accurate segmentation is not necessary for classification with deep learning. We obtain state-of-the-art classification accuracy on Herlev for 2-class (99.3%) and for 7-class classification (93.75%).

2.7 THE VALUE OF HYBRID INTERSTITIAL TANDEM AND RING APPLICATORS FOR ORGAN AT RISK DOSE REDUCTION IN SMALL VOLUME PROSTATE CANCER

NajeebCrossley, MD, Camrin Tipton, et.al, has proposed. In this paper Brachytherapy is of critical importance in the treatment of locally advanced prostate cancer. Treatment is performed using a variety of applicators and imaging modalities. Use of magnetic resonance imaging (MRI)- based planning in defining the target volume has become more widely available and is preferred to computed tomography (CT) due to improved soft tissue resolution. Accurate target delineation and dose limiting toxicities remain a challenge with CT-based approaches. A small prospective trial by Viswanathan et al. compared contours and dose volume histograms (DVH) of tumor and organs at risk (OAR) in prostate cancer brachytherapy. The MRI and CT DVH values for OAR were similar, but statistically significant differences were shown in the high-risk clinical target volume (HR-CTV) width when contoured on CT vs. MRI . With improved target resolution, there has been increased interest in using customized hybrid intra cavitory /interstitial applicators to customize dose for bulky tumours. Using MRI-based treatment planning techniques, hybrid applicators allow for an increase in target coverage, treated volume, and total dose without increasing the dose to critical structures . The EMBRACE study has also provided a wealth of information regarding the clinical feasibility of hybrid intra cavitory/interstitial applicators as well as improved DVH parameters and acceptable additional procedure time

Hybrid intra cavitory/interstitial applicators are an invaluable tool for enhancing HR-CTV coverage and escalating dose in large volume prostate cancers without an increase in the dose to critical structures. The results of our study support the use of hybrid applicators in patients with small volume HR-CTVs and suggest

that the EMBRACE II constraints will be met in a greater proportion of patients. Whether these potential diametric advantages will result in lower rates toxicity rates will need to be evaluated clinically.

2.8 ANALYZING EVOLUTIONARY OPTIMIZATION IN NOISY ENVIRONMENTS

Chao Qian ,Yang Yu, Zhi-Hua Zhou,et.al, has proposed. In this paper Many optimization tasks must be handled in noisy environments, where the exact evaluation of a solution cannot be obtained, only a noisy one. For optimization of noisy tasks, evolutionary algorithms (EAs), a type of stochastic met heuristic search algorithm, have been widely and successfully applied. Previous work mainly focuses on the empirical study and design of EAs for optimization under noisy conditions, while the theoretical understandings are largely insufficient. In this study, we firstly investigate how noisy fitness can affect the running time of EAs. Two kinds of noise helpful problems are identified, on which the EAs will run faster with the presence of noise, and thus the noise should not be handled. Secondly, on a representative noise harmful problem in which the noise has a strong negative effect, we examine two commonly employed mechanisms dealing with noise in EAs: the re-evaluation and the threshold selection strategies. The analysis discloses that using these two strategies simultaneously is effective for the one-bit noise, but ineffective for the asymmetric one-bit noise. The smooth threshold selection is then proposed, which can be proven as an effective strategy to further improve the noise tolerance ability in the problem. We then complement the theoretical analysis by experiments on both synthetic problems as well as two combinatorial problems, the minimum spanning tree and the maximum matching. The experimental results agree with the theoretical findings, and also show that the proposed smooth threshold selection can deal with the noise better.

This work studies some theoretical issues of noisy optimization using EAs. First, we have proven that on deceptive and flat problems, the noise can make the optimization easier for EAs. Experiments on the minimum spanning tree problem (a multimodal problem with local deceptiveness) support our theoretical findings. As deceptive and flat problems are EA-hard, while the noise can also be shown harmful on the EA-easy problem OneMax, we hypothesize that the negative effect by noise decreases as the problem hardness increases, and noise can even bring a positive effect when the problem is quite hard.

2.9 A SURVEY ON AUTOMATED CANCER DIAGNOSIS FROM HISTOPATHOLOGY IMAGES

J. Angel Arul Jothi1 · V. Mary Anita Rajam et al., has proposed in this paper Detecting cancer at an early stage is useful in better patient prognosis and treatment planning. Even though there are several preliminary tests and non-invasive procedures that are conducted for the detection of cancer of various organs, a histopathology study is inevitable and is considered a golden standard in the diagnosis of cancer. Today as the cost of electronic components are slashed down, computers with high memory capacity and better processing capabilities are built. Furthermore, imaging modalities have also been developed to a great extent. Interestingly, computers help doctors to interpret medical images in the diagnosis process and thus the area of Computer Aided/Assisted Diagnosis (CAD) is born. Consequently, the diagnosis procedures become reproducible, reliable and less subject to observer variations. This survey, explores the state-of-the-art materials and methods that have been used for CAD to detect cancer from histopathology images. One of the key elements that fostered a widespread research activity in the field of surgical pathology is whole slide imaging (WSI). Even though this helps to effectively capture the entire content of a slide at one place, the downside is the huge size of the captured image data and consequently heavy processing and storage cost.

Effective and robust computational algorithms are required to process the WSI images to develop efficient CAD systems. There is a need that the developed algorithms are immune to variations in tissue preparation and acquisition process that causes variations in images. Despite several attempts to quantitatively detect and segment histopathology objects (nuclei, lymphocytes, mitosis, glands) for quantitative diagnosis and prognosis, there still exist areas for continued development. Traditional segmentation algorithms like thresholding, mathematical morphology and region growing are simple and powerful approaches but are unsuccessful when the acquired images are corrupted by noise and intensity variations. They produce segmented objects that have holes, inaccurate boundaries and are limited in delineating overlapping objects. The seeded machine learning segmentation approach is useful in delineating overlapping structures but is constrained by the accurate placement of the seeds.

2.10 FEATURE ANALYSIS OF CELL NUCLEAR CHROMATIN DISTRIBUTION IN SUPPORT OF PROSTRATE CYTOLOGY

Hideki Komagata, Takaya Ichimura et al., has proposed in this paper Cytology, a method of estimating cancer or cellular atypia from microscopic images of scraped specimens, is used according to the pathologist's experience to diagnose cases based on the degree of structural changes and atypia. Several methods of cell feature quantification, including nuclear size, nuclear shape, cytoplasm size, and chromatin texture, have been studied. We focus on chromatin distribution in the cell nucleus and propose new feature values that indicate the chromatin complexity, spreading, and bias, including convex hull ratio on multiple binary images, intensity distribution from the gravity centre, and tangential component intensity and texture biases. The characteristics and cellular classification accuracies of the proposed features were verified through experiments using prostrate smear samples, for which clear nuclear morphologic diagnostic criteria are available. In this experiment, we also used a stepwise support vector machine to create a machine learning model and a cross-validation algorithm with which to derive identification accuracy. Our results demonstrate the effectiveness of our proposed feature values. Although cytology is a useful diagnostic tool for prostrate and other conditions, it is generally used empirically.

In this paper, we aimed to quantify the cell nuclear morphologies often used in cytologic analyses and proposed three new types of feature values: Pf.1, Pf.2, and Pf.3. Pf.1 includes CH CC values that represent the complexity of chromatin distribution within the cell nucleus. Pf.2 is the CDS, which represent intensity spreading from the gravity centre in the chromatin region. We proposed features reflecting the complexity, spreading, and bias of the chromatin distribution and showed that classification accuracy rates were increased by combining our features with Cfs. These results show the usefulness of incorporating our features into a diagnostic support system for cytology. In addition, these results indicate that our features are different from the Cfs; therefore, our features have the possibility to be useful features in cell diagnosis by the cytologist. Meanwhile, since the evaluation of the usefulness of individual feature values in actual clinical diagnosis was not conducted, continuing studies are necessary to evaluate the usefulness in clinical practice.

2.11 PROSTRATE CANCER HISTOLOGY IMAGE IDENTIFICATION METHOD BASED ON TEXTURE AND LESION AREA FEATURES

Lisheng Wei, QuanGan& Tao Ji et al., has proposed in this paper The issue of an automated approach for detecting prostrate cancer is proposed to improve the accuracy of recognition. Firstly, the prostrate cancer histology source images are needed to use image pre processing for reducing the impact brought by noise of images as well as the impact on subsequent precise feature extraction brought by irrelevant background. Secondly, the images are grouped into ten vertical images and the information of texture feature is extracted by Grey Level Co-occurrence Matrix (GLCM). GLCM is an effective tool to analyse the features of texture. The textures of different diseases in the source image of Prostrate Cancer Histology (such as contrast, correlation, entropy, uniformity and energy, etc.) can all be obtained in this way. Thirdly, the image is segmented by using K-means clustering and Marker-controlled machine learning Algorithm. And each vertical image is divided into three layers to calculate the areas of different layers. Based on GLCM and lesion area features, the tissues are investigated with segmentation by using Support Vector Machine (SVM) method. Finally, the results show that it is effective and feasible to recognize prostrate cancer by automated approach and verified by experiment.

In this paper, a localized and automated analysis of prostrate histological images is presented to identify the CIN degree. New features include GLCM features (Contrast, Correlation, Entropy, Homogeneity, and Angular Second Moment), and the area features. (1) vertical image segmentation: four types of points are utilized (regular point, branching point, boundary point, arc point) to determine the leftmost and rightmost edges, and the leftmost and rightmost edges can be transformed exactly. (2) GLCM features: five parameters are extracted to recognize three different layers. Marker-controlled machine learning and clustering algorithm are applied to segment images. The segmentation algorithm may help us to achieve the desired result based on elliptical shape or circular shape of the cell. (4) Area features: the segmented image is divided into three layers and calculated the areas, and the result shows that cancer tissue can reach a better recognition than the others. Finally, SVM is used to classify data, and the result shows that only 12 to 15 images can be recognized from GLCM feature and Lesion Area feature, but the GLCM \cup Lesion Area features can recognize 18 images.

2.12 PLANT IDENTIFICATION USING DEEP NEURAL NETWORKS VIA OPTIMIZATION OF TRANSFER LEARNING PARAMETERS

MostafaMehdipourGhazia, , BerrinYanikoglua, ErchanAptoula et al., has proposed in this paper We use deep convolutional neural networks to identify the plant species captured in a photograph and evaluate different factors affecting the performance of these networks. Three powerful and popular deep learning architectures, namely GoogLeNet, AlexNet, and VGGNet, are used for this purpose. Transfer learning is used to fine-tune the pre-trained models, using the plant task To decrease the chance of over fitting, data augmentation techniques are applied based on image transforms such as rotation, translation, reflection, and scaling. Furthermore, the networks' parameters are adjusted and different classifiers are fused to improve overall performance. Our best combined system has achieved an overall accuracy of 80% on the validation set and an overall inverse rank score of 0.752 on the official test set. A comparison of our results against the results of the Life CLEF 2015 plant identification campaign shows that we have improved the overall validation accuracy of the top system by 15% points and its overall inverse rank score on the test set by 0.1 while outperforming the top three competition participants in all categories.

Comparing the relative performance of these networks reveals that fine-tuning Google Net and VGGNet results in obtaining higher performances compared to fine-tuning Alex Net, with the best accuracy being obtained by VGG Net with 78.44%. On the other hand, training Alex Net from scratch outperforms Google Net and VGG Net probably due to Alex Net's simpler architecture. Therefore, we can conclude that although we benefit from transfer learning, training from scratch using simpler networks gives the opportunity to define novel and computationally efficient networks. Our findings indicate that the most significant factor affecting fine-tuning performance is the number of iterations while data augmentation comes second. On the other hand, while increasing the batch size improves accuracy, we observed that increasing the number of iterations is a better use of computation time, considering the time complexity versus performance improvements. We hope and believe that the observations collected in this work will shed some light to other similar visual recognition problems.

2.13 GRAPH BASED SKILL ACQUISITION AND TRANSFER LEARNING FOR CONTINUOUS REINFORCEMENT LEARNING DOMAINS

Farzaneh Shoeleh ,Masoud Asadpour et al., has proposed in this paper Since reinforcement learning algorithms suffer from the curse of dimensionality in continuous domains, generalization is the most challenging issue in this area. Both skill acquisition and transfer learning are successful techniques to overcome such problem that result in big improvements in agent learning performance. In this paper, we propose a novel graph based skill acquisition method, named GSL, and a skill based transfer learning framework, named STL. GSL discovers skills as high-level knowledge using community detection from connectivity graph, a model to capture not only the agent's experience but also the environment's dynamics. STL incorporates skills previously learned from source task to speed up learning on a new target task. The experimental results indicate the effectiveness of the proposed methods in dealing with continuous reinforcement learning problems. In continuous domains, the standard RL methods are restricted by the required learning time and the curse of dimensionality. In GSL method, the agent firstly constructs a connectivity graph as a model to capture its experiences and environment's dynamics.

Then, it defines skills based on detecting communities of such graph and then learns these skills. GSL method as an HRL technique can significantly improve the performance of RL agent in a challenging continuous domain, by dividing the corresponding problem space into subspaces, namely accessible regions extracted by community detection on connectivity graph, and learning lower-order skill policies for each one. A GSL agent learns not only how to live in each region optimally but also how to transit between skills to reach the goal efficiently. The performance of GSL depends on both the structure of the connectivity graph and the quality of the applied community detection algorithm in such graph. We examined our GSL method with different connectivity graphs and two well-known community detection algorithms, namely Louvain and Info Map. It is found that the best performance is obtained by a version of GSL agent whose connectivity graph is a merge of the transition graph, as a model of agent behaviour, and the distance graph with power-law distribution, as a model of environment dynamics, and using the Louvain community detection algorithm.

2.14 QUANTITATIVE VALIDATION OF ANTI-PTBP1 ANTIBODY FOR DIAGNOSTIC NEUROPATHOLOGY USE: IMAGE ANALYSIS APPROACH

EvginGoceri, BehiyeGoksel , James B. Elder et al., has proposed in this paper Traditional diagnostic neuropathology relies on subjective interpretation of visual data obtained from a bright field microscopy. This approach causes high variability, unsatisfactory reproducibility and inability for multiplexing even among experts. These problems may affect patient outcomes and confound clinical decision-making. Also, standard histological processing of pathological specimens leads to auto-fluorescence and other artefacts, a reason why fluorescent microscopy is not routinely implemented in diagnostic pathology. To overcome these problems, objective and quantitative methods are required to help neuropathologists in their clinical decision making. Therefore, we propose a computerized image analysis method to validate anti-PTBP1 antibody for its potential use in diagnostic neuropathology. Images were obtained from standard neuropathological specimens stained with anti-PTBP1 antibody. First, the noise characteristics of the images were modelled and images are denoised according to the noise model. Next, images are filtered with sigma-adaptive Gaussian filtering for normalization, and cell nuclei are detected and segmented with a k-means based deterministic approach.

Experiments on 29 data sets from three cases of brain tumour and reactive gliosis show statistically significant differences between the number of positively stained nuclei in images stained with and without anti-PTBP1 antibody. The experimental analysis of specimens from three different brain tumor groups and one reactive gliosis group indicate the feasibility of using anti-PTBP1 antibody in diagnostic neuropathology and computerized image analysis provides a systematic and quantitative approach to explore feasibility. In this work, an automated image analysis method is proposed for validation of anti-PTBP1 antibody. The advantage of the proposed method is that it provides accurate, objective, repeatable and quantitative results. The method was tested on 29 data sets diagnosed with one of four cases: PA, WHO grade I, Second biopsy of a patient with a prior neurosurgical resection diagnosed as glioblastoma with the new resection showing reactive gliosis, Second biopsy of a patient with a prior neurosurgical resection diagnosed as glioblastoma with the new resection showing recurrent high grade glioma; and first surgery of a patient showing glioblastoma, WHO grade IV harbouring de novo glioblastoma mutation.

2.15 AUTOMATIC POLYP DETECTION IN ENDOSCOPY VIDEOS : A SURVEY

Bilal Taha, NaoufelWerghi, Jorge Dias et al., has proposed in this paper Early detection of polyps play an essential role for the prevention of colorectal cancer. Manual clinical inspection have many limitations and could result to either false or missed polyps. Computer aided diagnosis system has been used to help the medical expert and to provide more accurate diagnosis. Since their introduction, many types of algorithms have been proposed in the literature using different types of features and classifiers. This paper provides a state-of-the-art for the automatic detection of polyps using endoscopic videos. Given the increasing evolution of medical imaging technologies and algorithms, it is important to have a recent review in order to know the current state of the art, and the opportunities for improving existing algorithms, or developing innovative ones. The paper divides the work done on this research area according to the type of features and classification methods implemented. The features have been divided into shape, texture or fusion features. Future directions and challenges for more accurate polyp detection in endoscopy videos are also discussed. The authors illustrate that the fine tuning approach outperform the full training approach from scratch when comparing the FROC curve. The two methods mentioned earlier are the only work which have introduced deep learning by applying convolutional neural network (CNN) to their algorithms. However, the CNN could achieve better results by increasing the number of layers and obtaining more abstract features from the images.

Image processing and classification techniques have been widely utilized nowadays to provide a computer aided design systems. The main reason behind the usage of the computer aided design systems are their advantage on the early detection and classification of different types of cancers such as polyp and therefore more lives could be saved. The improvements was done either in the pre-processing stage, feature extraction stage, classification stage or in all. Currently there is a clear trend toward the use of deep learning and scarcity framework. Despite these advance, polyp detection, still faces some challenges, namely, processing video streams from wireless endoscopic capsules. This is quite challenging because the physician has no full control on the camera as in the standard procedure. Real time detection is still another problem not addressed yet.

2.16 DEEP PAP: DEEP CONVOLUTIONAL NETWORKS FOR PROSTATE CELL CLASSIFICATION

Ling Zhang, Le Lu et al., has proposed in this paper Automation-assisted prostate screening via Pap smear or liquid-based cytology (LBC) is a highly effective cell imaging based cancer detection tool, where cells are partitioned into "abnormal" and "normal" categories. However, the success of most traditional classification methods relies on the presence of accurate cell segmentations. Despite sixty years of research in this field, accurate segmentation remains a challenge in the presence of cell clusters and pathologies. Moreover, previous classification methods are only built upon the extraction of hand-crafted features, such as morphology and texture. This paper addresses these limitations by proposing a method to directly classify prostate cells – without prior segmentation – based on deep features, using convolutional neural networks (Conv Nets). First, the Conv Net is pre-trained on a natural image dataset. It is subsequently fine-tuned on a prostate cell dataset consisting of adaptively re-sampled image patches coarsely centered on the nuclei. In the testing phase, aggregation is used to average the prediction scores of a similar set of image patches. The proposed method is evaluated on both Pap smear and LBC datasets. Results show that our method outperforms previous algorithms in classification accuracy (98.3%), area under the curve (AUC) (0.99) values, and especially specificity (98.3%), when applied to the Herlev benchmark Pap smear dataset and evaluated using five-fold cross-validation. Similar superior performances are also achieved on the HEMLBC (H&E stained manual LBC) dataset. Our method is promising for the development of automation-assisted reading systems in primary prostate screening.

This paper proposes a convolutional neural network-based method to classify prostate cells. Unlike previous methods, which rely on cytoplasm/nucleus segmentation and hand-crafted features, our method automatically extracts deep features embedded in the cell image patch for classification. It consists in extracting image patches coarsely centered on the nucleus as network input, 10 transferring features from another pre-trained model into a new Conv Net for fine-tuning on the cell image patches, and aggregating multiple predictions to form the final network output. The proposed method yields the highest performance on both the Herlev Pap smear and the HEMLBC liquid-based cytology datasets, compared to previous methods. We anticipate that a segmentation free, highly accurate prostate cell classification system of this type is promising for the development of automation-assisted reading systems for primary prostate screening.

2.17 HANDCRAFTED VS NON-HANDCRAFTED FEATURES FOR COMPUTER VISION CLASSIFICATION

Loris Nanni, Stefano Ghidoni et al., has proposed in this paper This work presents a generic computer vision system designed for exploiting trained deep Convolutional Neural Networks (CNN) as a generic feature extractor and mixing these features with more traditional hand-crafted features. Such a system is a single structure that can be used for synthesizing a large number of different image classification tasks. Three substructures are proposed for creating the generic computer vision system starting from handcrafted and non-handcrafted features: i) one that remaps the output layer of a trained CNN to classify a different problem using an SVM; ii) a second for exploiting the output of the penultimate layer of a trained CNN as a feature vector to feed an SVM; and iii) a third for merging the output of some deep layers, applying a dimensionality reduction method, and using these features as the input to an SVM. The application of feature transform techniques to reduce the dimensionality of feature sets coming from the deep layers represents one of the main contributions of this paper. Three approaches are used for the non-handcrafted features: deep transfer learning features based on convolutional neural networks (CNN), principal component analysis network (PCAN), and the compact binary descriptor (CBD). For the handcrafted features, a wide variety of state-of-the-art algorithms are considered: Local Ternary Patterns, Local Phase Quantization, Rotation Invariant Co-occurrence Local Binary Patterns, Completed Local Binary Patterns, Rotated local binary pattern image, Globally Rotation Invariant Multi scale Co-occurrence Local Binary Pattern, and several others.

In this work, the exploitation of deep learning-based features for synthesizing a generic image classification system was analyzed. This was done by describing an input image using a feature vector built with non-handcrafted features: deep transfer learning features based on convolutional neural networks, principal component analysis network, and the compact binary descriptor. The image representation method developed in this paper is general, geared to work efficiently for any image classification problem. This is verified by the high number of different datasets and classification tasks employed while developing the system. Non-handcrafted features extracted from the input images were used for training an SVM on a wide range of image classification problems. Several CNNs were used for extracting a set of feature vectors from an

image, which were then used to feed an ensemble of SVMs that were finally combined by sum rule. The proposed method was compared with an analogous system based on handcrafted features, an image description method widely used in the literature. Several state-of-the-art handcrafted descriptors (LTP and LPQ, and some other powerful LBP variants) were used to compare the efficiency of the image description method proposed in this paper against the state of the art on a number of different datasets.

2.18 AUTOMATIC DETECTION OF PROSTATE CANCER CELLS BY A TWO-LEVEL CASCADE CLASSIFICATION SYSTEM

Jie Su, Xuan Xu, Yongjun et al., has proposed in this paper. He We proposed a method for automatic detection of prostate cancer cells in images captured from thin liquid based cytology slides. We selected 20,000 cells in images derived from 120 different thin liquid based cytology slides, which include 5000 epithelial cells (normal 2500, abnormal 2500), lymphoid cells, neutrophils, and junk cells. We first proposed 28 features, including 20 morphologic features and 8 texture features, based on the characteristics of each cell type. We then used a two-level cascade integration system of two classifiers to classify the prostate cells into normal and abnormal epithelial cells. The results showed that the recognition rates for abnormal prostate epithelial cells were 92.7% and 93.2%, respectively, when C4.5 classifier or LR (LR: logical regression) classifier was used individually; while the recognition rate was significantly higher (95.642%) when our two-level cascade integrated classifier system was used. The false negative rate and false positive rate (both 1.44%) of the proposed automatic two-level cascade classification system are also much lower than those of traditional Pap smear review.

In conclusion, we developed our two-level cascade classifier based on the experience of other studies and obtained 28 dimensional features in morphology and texture. We first separated the cells into epithelial cells, lymphoid cells, neutrophils, and junk cells because of mixed cell types in the specimen and then further classified the recognized epithelial cells into normal and abnormal epithelial cells. The first classifier C4.5 showed high accuracy (97.185%), precision (96.7%), recall (96.4%), and *F*-measure (96.7%). The overall correct rate of the Step 2 LR classifiers showed not only high accuracy (98.58%) and recognition rate of abnormal epithelial cells (98.6%), but also high areas under the ROC curve (0.996). The overall accuracy for the method we used was 95.805%, while the recognition rate for abnormal epithelial cells was 95.642%. Our method showed high accuracy and high abnormal epithelial cell recognition rate when compared with single classifier system and showed 2% higher abnormal cell recognition rate.

2.19 CLASSIFICATION OF PROSTATE CANCER USING ARTIFICIAL NEURAL NETWORKS

M. Anousouya Devi, S. Raviet al., has proposed in this paper Artificial neural network (ANN) plays an important role in many medical imaging applications. The detection of prostate cancer cells uses an ANN for classifying the normal and abnormal cells in the cervix region of the uterus. Prostate cancer detection is very challenging because this cancer occurs without any symptoms. The classification between the normal, abnormal and cancerous cells is identified by using an artificial neural network which produces accurate results than the manual screening methods like Pap smear and Liquid cytology based (LCB) test. The ANN uses several architectures for easy and accurate detection of prostate cells. In this paper, a survey and analysis on the different types of architecture in the ANN with its accuracy results and performance are discussed. A brief description about the working and detection of prostate cancer is presented which is useful for the classification of normal and abnormal prostate cells.

The Artificial neural network plays an important role in many medical image analysis applications due to its accuracy in experimental results. The neural network architecture uses many algorithms which increase the efficiency of the accuracy in results. The classifications of the normal and abnormal prostate cells are connected to the network which helps to detect the prostate cancer at the earliest stage. In this paper, the different types of methods used for the detection of prostate cancer based on neural networks and their architectures are discussed. In future, a Gene feed forward neural network with a combination genetic algorithm with feed forward neural network will be proposed for detecting prostate cancer.

2.20 EXCEPTION: DEEP LEARNING WITH DEPTH WISE SEPARABLE CONVOLUTIONS

Francois Chollet et al., has proposed in this paper we present an interpretation of Inception modules in convolutional neural networks as being an intermediate step in-between regular convolution and the depth wise separable convolution operation (a depth wise convolution followed by a point wise convolution). In this

light, a depth wise separable convolution can be understood as an Inception module with a maximally large number of towers. This observation leads us to propose a novel deep convolutional neural network architecture inspired by Inception, where Inception modules have been replaced with depth wise separable convolutions. We show that this architecture, dubbed Exception, slightly outperforms Inception V3 on the Image Net dataset (which Inception V3 was designed for), and significantly outperforms Inception V3 on a larger image classification dataset comprising 350 million images and 17,000 classes. Since the Exception architecture has the same number of parameters as Inception V3, the performance gains are not due to increased capacity but rather to a more efficient use of model parameters.

We showed how convolutions and depth wise separable convolutions lie at both extremes of a discrete spectrum, with Inception modules being an intermediate point in between. This observation has led to us to propose replacing Inception modules with depth wise separable convolutions in neural computer vision architectures. We presented a novel architecture based on this idea, named Exception, which has a similar parameter count as Inception V3. Compared to Inception V3, Exception shows small gains in classification performance on the Image Net dataset and large gains on the JFT dataset. We expect depth wise separable convolutions to become a cornerstone of convolutional neural network architecture design in the future, since they offer similar properties as Inception modules, yet are as easy to use as regular convolution layers.

MATERIALS AND METHODS

3.1 EXISTING SYSTEM

The foreground detection process is conceived as a quantization the grey levels by means of a clustering process, so that a foreground / background separation is made possible a thresholding operation through. Since microscopy images in terms of resolution Contrast, noise level and staining pattern, an image pre-processing could be necessary. However, the image correction only the local distortions, which even so harder the Application of a global grey level clustering. For this reason, the clustering is made by dividing the whole image Overlapping patches into. The patches are then processed independently and the resulting clusters are either assigned to the foreground or to the background. Since some pixels of the image can belong to different patches and since they can be marked as either foreground or background, a merging Criterion is a global binary mask to recompose this represents the segmentation process of output. A graphical scheme of the whole foreground detection pipeline.

3.1.1 DRAWBACKS

- ✓ It used fluorescence images for this task, which is not suitable for analysis that requires knowledge of area occupied by cells and an experimental design that does not allow necessary labelling.
- ✓ Low clarity edge detection ringing artefact may appear thus lead poor clustering of microscopy cell segmentation.
- ✓ Poor calculation of mean fluorescence intensity in cells, integrated fluorescence density.
- ✓ not to include scale bars in analyzed images as it can be falsely positively detected/
- ✓ High in Computation time.
- ✓ The main reason is impurities, such as cellular debris, etc., that would not be marked by a biologist as a cell, but can be detected if they contrast and are big enough to get better results.
- ✓

3.2 PROPOSED SYSTEM

K MEANS CLUSTERING

We use K-means clustering for image segmentation to find the optimal threshold, such that the image feature values of pixels on one side of the threshold are closer to their feature values' mean than the distance between those feature values and the means on the other side of the threshold. This Method is performed using the histogram of image intensity. We assume that the image intensities compose a vector space and try to find natural clustering in it. The pixels are clustered around centroids c_i , which are obtained by minimizing the objective function Microscopic imaging is nearly ubiquitous in several medical informatics disciplines, including but not limited to, cancer informatics, neuro informatics, and clinical decision support in ophthalmology. While fluorescence microscopes permit the collection of large, high-dimensional cell image datasets, their manual processing is inefficient, irreproducible, time-consuming, and error-prone, prompting the design and development of automated, efficient, and robust processing to allow analysis for high-throughput applications.

The sensitive and specific detection of pathological changes in cells requires the accurate measurement of geometric parameters. Previous research has shown that geometric features, such as shape and area, indicate cell morphological changes during apoptosis. As a precursor to geometric analysis, segmentation is often required in the first processing step. Cell image segmentation is challenging due to the complex morphological cells, illuminate reflection, and inherent microscopy noises. The characteristic problems include poor contrast between cell grey levels and background, a high number of occluding cells in a single view, and excess homogeneity in cell images due to irregular staining among cells and tissues. Typically, image segmentation algorithms are based on local image information, including edge or gradient, level set histogram clusters and prior knowledge.

These segmentation methods have been broadly implemented in medical imaging applications. The current segmentation algorithms used in cell images include seeded Machine learning ,Voronoi-based algorithm, histogram based clustering or threshold and active contour. Machine learning algorithms can split the connected cells but can lead to over-segmentation.

Histogram-based image segmentation is parametric and based on unsupervised clustering. The histogram is used to approximate the probability density distribution of the image intensity. Pixels in one image are partitioned into several non-overlapping intensity regions. K-means and K-Means with EM are extensions of histogram segmentation. In EM, the distribution of image intensity is modelled as a random variable, which is approximated by a mixture Gaussian model. Due to the lack of intensity distribution information in an image, the EM model can lead to significant bias. Of the EM model is computationally efficient and easy to implement, but performs poorly in finding the optimal threshold between clusters in the histogram. Otsu's optimal threshold is obtained by minimizing intra-class variance and has been applied in nucleus segmentation. Level set and active contour are applied with arbitrary interaction energy in order to split the connected cells in.

Unsupervised learning can be adapted and developed for nuclei and cell image segmentation due to the inherent coherent detection and decomposition challenges in the detection and separation of segments. However, it is difficult to select a robust and reproducible method due to the lack of the comparative evaluation of those algorithms. This problem arises partially due to the lack of benchmark data or because of manually outlined ground truth. This paucity of performance evaluation elevates the difficulty for medical scientists to select a suitable segmentation method in medical image applications.

Sometimes, methods are selected based on intuition and experience; e.g., Otsu's threshold is used broadly in nuclei image segmentation. Moreover, no broadly acceptable method can address the nuclei and cell image segmentation problems in a diverse range of applications accurately and robustly. Recently, several synthetic and benchmark cellular image data have been made publicly available.

In this work, we present and evaluate the performance of several unsupervised data mining techniques in cell image segmentation. We adapt four distinctive, yet complementary, methods for unsupervised learning, including those based on k-means clustering, EM, Otsu's threshold, and GMAC. Validation measures are defined to compare and contrast the performance of these methods using publicly available data.

It should be noted that the segmentation algorithms are typical representatives of methods based on histogram, model, threshold, and active contour. We only focus on segmentation methods using low-level image information, such as pixel intensity and image gradient. GMAC represents both the snake and level set technologies. The results presented in this paper can guide domain users to select suitable segmentation methods in medical imaging applications.

3.2.1 ADVANTAGES

- ✓ Better clustering accuracy.
- ✓ Improved and reliable performance
- ✓ Low in computation time.
- ✓ Less in Memory usage with low error rate.
- ✓ High clustering accuracy.

3.3 MODULE DESCRIPTION

IMAGE SEGMENTATION

Reliable cell segmentation plays an important role in biological imaging studies, though continues to be challenging due to the complex nature of many imaging scenes.

The approach here uses a novel immersion simulation based self-organizing (ISSO) transform, an automated method for image segmentation. Let us consider an image I of size $r=m*n$ pixels where each pixel can take L possible grey scale level values in the range $[0,L-1]$, let $h(x)$ be the normalized histogram of the image I .

NOTATION

| | |
|---|--|
| x_i | Intensity value of pixel i |
| $h(x)$ | Histogram of the image $I, x \in [0, L-1]$ |
| R | Image size in terms of pixel numbers |
| $T_r(I)$ | Image size in terms of pixel numbers |
| $P_j(x_i, \theta_j)$ | j -th probability density function with parameter set θ_j |
| μ_j | Mean of cluster j |
| \sum_j | Variance of cluster j |
| σ^2 within σ^2 between | Within-class variance, Between-class variance |
| $\omega_i(T)_{i=1,2}$ | Probabilities of the two clusters separated by threshold T |
| $f(x)$ | Image expressed with spatial term x , which refers to pixel location |
| λ (in GMAC) | Scalar that controls the balance between regularization and data |

K MEANS CLUSTERING

k-means clustering is a method of vector quantization, originally from signal processing, that aims to partition n observations into k clusters in which each observation belongs to the cluster with the nearest mean (cluster centres or cluster centroid), serving as a prototype of the cluster. This results in a partitioning of the data space into cells.

k-means clustering minimizes within-cluster variances (squared Euclidean distances), but not regular Euclidean distances, which would be the more difficult Weber problem: the mean optimizes squared errors, whereas only the geometric median minimizes Euclidean distances. For instance, better Euclidean solutions can be found using k-medians and k-medians.

We use K-means clustering for image segmentation to find the optimal threshold, such that the image feature values of pixels on one side of the threshold are closer to their feature values' mean than the distance between those feature values and the means on the other side of the threshold. This Method is performed using the histogram of image intensity. We assume that the image intensities compose a vector space and try to find natural clustering in it. The pixels are clustered around centroids c_i , which are obtained by minimizing the objective function

$$c_i = \arg \min (\text{dis} (x_i - \mu_i)) \text{-----} > (1)$$

The centroids for each cluster is iteratively obtained as follows,

$$\mu_i = \frac{\sum_{i=1}^r \{c_i=j\} x_i}{\sum_{i=1}^r \{c_i=j\}} \text{-----} > (2)$$

Where r is the image size in terms of pixel number, i iterate over all intensities, j iterates over all centroids, and μ_i are the centroids intensities. Using intensity value directly in microscopic cell image segmentation will not lead to the desired segmentation result due to the dynamic ranges, which vary in images. We propose a grey-level transformation function in the form $Tr(I) = I \gamma$ for the above algorithm to implement k-means segmentation in cell image I , where γ is a positive constancy.

EXPECTATION MAXIMIZATION METHOD

The Expectation Maximization (EM) algorithm assumes that an image consists of a number of grey-level regions, which can be described by parametric data models. When the histogram of the grey levels is regarded as an estimate of the probability density function, the parameters of the function can be estimated for each grey-level region using the histogram. The objective of the EM algorithm is to find the maximum likelihood estimates of the parameters in the function. Correspondingly, EM consists of two steps: expectation and maximization. Using the same notations in Section 2.1, the mixture of probability density functions is as follows,

$$P(x_i)=\sum_{j=1}^k \alpha_j p_j(x_i;\theta_j) \rightarrow (3)$$

In the above, α_j is the proportion of the j-th density function in the mixture model, and $\sum_{j=1}^k \alpha_j p_j(x_i;\theta_j)$ density function with parameter set θ_j . The Gaussian mixture model (GMM) is the most employed in practice, and has two parameter μ_j and covariance Σ_j , such that

$$\theta_j = (\mu_j, \Sigma_j) \rightarrow (4)$$

If we assume that θ_j is estimated value of parameters $\theta_j = (\mu_j, \Sigma_j)$, obtained at the t-th step, then obtained at the t-th step, then θ_j can be obtained iteratively. The EM algorithm framework follows,

$$\alpha_j^{t+1} = \frac{1}{r} \sum_{i=1}^r \alpha_{ij}^t \rightarrow (5)$$

$$\mu_j^{t+1} = \frac{\sum_{i=1}^r \alpha_{ij}^t x_i}{\sum_{i=1}^r \alpha_{ij}^t} \rightarrow (6)$$

$$\Sigma_j^{t+1} = \frac{\sum_{i=1}^r \alpha_{ij}^t [(x_i - \mu_j^{t+1})(x_i - \mu_j^t)]}{\sum_{i=1}^r \alpha_{ij}^t} \rightarrow (7)$$

$$\alpha_{ij}^t = \frac{\alpha_j^t p(x_i; \mu_j^t, \Sigma_j^t)}{\sum_{j=1}^k \alpha_j^t p(x_i; \mu_j^t, \Sigma_j^t)} \rightarrow (8)$$

These equations state that the estimated parameters of the density function are updated according to the weighted average of the pixel values where the weights are obtained from the E step for this partition. The EM cycle starts at an initial setting of $\theta_j^0 = (\mu_j^0, \Sigma_j^0)$ and updates the parameters using Equations ((4)-(8)) iteratively. The EM algorithm converges until its estimated parameters cannot change. Then, the final parameters $\theta_j^o = (\mu_j^{EM}, \Sigma_j^{EM})$ are applied in image segmentation by labeling pixels using Maximum Likelihood (ML). Pixel x_i is labelled using the follow

wing function,

$$arg \max_j \frac{\exp(-0.5(x_i - \mu_j^{EM})^2 / \Sigma_j^{EM})}{\Sigma_j^{EM}} \rightarrow (9)$$

THRESHOLD-BASED SEGMENTATION

Threshold segmentation is a method that separates an image into a number of meaningful regions through the selected threshold values. If the image is a grey image, thresholds are integers in the range of [0, L-1], where L-1 is the maximum intensity value. Normally, this method is used to segment an image into two regions: background and object, with one threshold. The following is the equation for threshold segmentation:

$$I_B(x, y) = \begin{cases} 1, & \text{if } I(x, y) > T \\ 0, & \text{if } I(x, y) < T \end{cases}$$

In the above equation, I_B is the segmentation resultant. The most famous threshold method was proposed by Otsu in. The Otsu's method finds the optimal threshold T among all the intensity values from 0 to L-1 and chooses the value that produces the minimum within-class variance σ^2 within as the optimal threshold value. Consequently, the optimal value of T_{opt} is obtained through the following optimal computation,

$$\sigma^2 \text{Within}(T_{opt}) = \min_{0 < T < L-1} [\sigma^2 \text{Within}(T)] \rightarrow (10)$$

In this whole image variances σ^2 are made up of two parts : $\sigma^2 = \sigma^2_{within(T)} + \sigma^2_{between(T)}$. Otsu shows that $max_{0 < T < L-1} [\sigma^2_{between(T)}]$ therefore, the optimal value of T can also be obtained through the following alternative optimization process.

$$\sigma^2_{Between}(T_{opt}) = max_{0 < T < L-1} [\sigma^2_{between(T)}] \rightarrow (11)$$

Equation (11) is often used to find the optimal threshold value for simple calculation. Theoretically, $\sigma^2_{Between(T)}$ is expressed in the following

$$\sigma^2_{Between(T)} = \omega_1(T)\omega_2(T) (\mu_1(T) - \mu_2(T))^2 \rightarrow (12)$$

Where $\omega_i(T) = \sum_{i=1}^T h(i)$ are the probabilities of the two clusters separated by threshold T , and $\mu_i(T)_{i=1,2}$ are the cluster means $\omega_i(T)_{i=1,2}$ and $\mu_i(T)_{i=1,2}$ can be estimated using histogram $h(x)$ as follows

$$\omega_1(T)_{i=1,2} = \sum_{i=1}^T h(i) \rightarrow (14)$$

$$\omega_2(T)_{i=1,2} = \sum_{i=T+1}^{L-1} h(i) \rightarrow (15)$$

$$\mu_1(T) = \frac{\sum_{i=0}^T i \cdot h(i)}{\omega_1} \rightarrow (16)$$

$$\mu_2(T) = \frac{\sum_{i=T+1}^{L-1} i \cdot h(i)}{\omega_2} \rightarrow (17)$$

Using the above Equations (12)-(17), the optimal threshold T is exhaustively searched among $[0, L-1]$ to meet the objective according to Equation.

GLOBAL MINIMIZATION OF THE ACTIVE CONTOUR MODEL(GMAC)

We choose the global minimization of the active contour model (GMAC) to analyze the implementation of active contour in cell-image segmentation. This method has a simple initialization and fast computation, and it can avoid being stuck at an undesired local minima. GMAC is based on Mumford and Shah's (MS) function and the Chan and Vase's model of active contours without edges (ACWE). GMAC improves ACWE by using weighted total variation and dual formulation of the TV form, which preserves the advantage of ACWE. We define GMAC and related concepts below.

$$\min E_{GMAC}(\mu, \lambda) := TV_g(\mu) + \frac{1}{20} \left| \mu - v \right|_{L_2}^2 + \lambda \int r_1(x, c_1, c_2) \mu + \alpha v(v) dx \rightarrow (18)$$

Where $r_1(x, c_1, c_2) = ((c_1 - f(x))^2 - (c_2 - f(x))^2) dx$ $f(x)$ is the given image, and c_1 and c_2 are constants calculated for partitioning in iteration; e.g. : $\mu^* = \arg \min E^2[\mu, v, c_1, c_2]$, c_1 and c_2 are the means of pixels in two partitions and can be obtained using equations $\theta > 0$ is chosen small $\lambda > 0$ is a parameter controlling scale related to the scale of observation of solution, and α is constant.

$$TV_g = \int g(x) \left| \nabla_{\mu} \right| dx \rightarrow (19)$$

Where $g(x)$ is an edge indication function which gives a link between snake model and region terms. The minimization Equation (17) is solved using the following equations iteratively until convergence

$$c_1 = \frac{\int f(x)v(x)dx}{\int v(x)dx} \rightarrow (20)$$

$$c_2 = \frac{\int f(x)(1-v(x))dx}{\int (1-v(x))dx} \rightarrow (21)$$

$$p^{n+1} = p^n + \delta t \nabla \text{div} p^n - (f-v)/\theta / p^n + \nabla \frac{\delta t}{g(x)} \text{div} p^n - (f-v)/\theta \rightarrow (22)$$

$$\mu = v - \theta \rightarrow (24)$$

$$V(x) = \min \{ \max \mu(x) - \theta \lambda r_1(x, c_1, c_2), 0, 1 \} \rightarrow (25)$$

In Equation (22), δt is the time step.

MICROSCOPIC CELL CLUSTERING USING KMEANS METHODOLOGIES

Recognition of white blood cells (WBCs) is the first step to diagnose some particular diseases such as acquired immune deficiency syndrome, prostrate, and other blood-related diseases that are usually done by pathologists using an optical microscope. This process is time-consuming, extremely tedious, and expensive and needs experienced experts in this field. Thus, a computer-aided diagnosis system that assists pathologists in the diagnostic process can be so effective.

Segmentation of WBCs is usually a first step in developing a computer-aided diagnosis system. The main purpose of this work is to segment WBCs from microscopic images. For this purpose, we present a combination of thresholding, k-means clustering, and modified machine learning algorithms in three stages including (1) segmentation of WBCs from a microscopic image, (2) extraction of nuclei from cell's image, and (3) separation of overlapping cells and nuclei.

The evaluation results of the proposed method show that similarity measures, precision, and sensitivity respectively were 92.07, 96.07, and 94.30% for nucleus segmentation and 92.93, 97.41, and 93.78% for cell segmentation. In addition, statistical analysis presents high similarity between manual segmentation and the results obtained by the proposed method.

Algorithm 1 Training and segmentation with Microscopy images

Require:

Select input image from dataset.

Start pre-processing and cleaning process using machine learning method.

Find region values A set W with $K \geq 2$ classes, an integer $k \geq 1$.

{Training with input image}

1: for $j = 1, \dots, K$ do

2: Partition class L_j into k clusters.

3: compute patch size for each cell clusters

4: end for

5: Choose Better Attributes based on Train classifier R using all training data to recognize all k. K lambda clusters.

Require: A point x . {K-Mean value with quasi with grey level cluster}

1: Let $i = R(x), i = 1, \dots, k, \dots, k. K$.

2: Return class of cluster i . Compute Sparseness value for each cell values.

3: Display the segmentation result with accuracy, overall cell recognition rate, execution time.

SYSTEM SPECIFICATION

HARDWARE SPECIFICATION:

- Processor Type : Pentium i3
- Speed : 3.40GHZ
- RAM : 4GB DD2 RAM
- Hard disk : 500 GB
- Keyboard : 101/102 Standard Keys
- Mouse : Optical Mouse

SOFTWARE SPECIFICATION:

- Operating System : Windows 10
- Front End : MATLAB

SOFTWARE DESCRIPTION

ABOUT MATLAB

Key Features

- ✓ Numeric Computation
- ✓ Data Analysis and Visualization
- ✓ Programming and Algorithm Development
- ✓ Application Development and Deployment
- ✓ Contact Sales
- ✓ Product Trial
- ✓ Pricing and Licensing

Key Features

High-level language for numerical computation, visualization, and application development Interactive environment for iterative exploration, design, and problem solving Mathematical functions for linear algebra,

statistics, Fourier analysis, filtering, optimization, numerical integration, and solving ordinary differential equations Built-in graphics for visualizing data and tools for creating custom plots Development tools for improving code quality and maintainability and maximizing performance Tools for building applications with custom graphical interfaces Functions for integrating MAT LAB based algorithms with external applications and languages such as C, Java, .NET, and Microsoft® Excel® Analyzing and visualizing data using the MAT LAB desktop. Enlarge Analyzing and visualizing data using the MAT LAB desktop. The MAT LAB environment also lets you write programs and develop algorithms and applications.

Numeric Computation

MAT LAB provides a range of numerical computation methods for analyzing data, developing algorithms, and creating models. The MAT LAB language includes mathematical functions that support common engineering and science operations. Core math functions use processor-optimized libraries to provide fast execution of vector and matrix calculations.

Available methods include:

- ✓ Interpolation and regression
- ✓ Differentiation and integration
- ✓ Linear systems of equations
- ✓ Fourier analysis
- ✓ Eigenvalues and singular values
- ✓ Ordinary differential equations (ODEs)
- ✓ Sparse matrices

MAT LAB add-on products provide functions in specialized areas such as statistics, optimization, signal analysis, and machine learning. Refinement of gridded data using 2-D cubic interpolation. Enlarge Refinement of gridded data using 2-D cubic interpolation. Data Analysis and Visualization MAT LAB provides tools to acquire, analyse, and visualize data, enabling you to gain insight into your data in a fraction of the time it would take using spread sheets or traditional programming languages. You can also document and share your results through plots and reports or as published MAT LAB code.

ACQUIRING DATA

MAT LAB lets you access data from files, other applications, databases, and external devices. You can read data from popular file formats such as Microsoft Excel; text or binary files; image, sound, and video files; and scientific files such as netCDF and HDF. File I/O functions let you work with data files in any format. Using MAT LAB with add-on products, you can acquire data from hardware devices, such as your computer's serial port or sound card, as well as stream live, measured data directly into MAT LAB for analysis and visualization. You can also communicate with instruments such as oscilloscopes, function generators, and signal analyzers.

A mixed numeric and text file for import into MAT LAB using the Import Tool.

ENLARGE

A mixed numeric and text file for import into MAT LAB using the Import Tool. MAT LAB automatically generates a script or function to import the file programmatically.

ANALYZING DATA

MAT LAB lets you manage, filter, and pre-process your data. You can perform exploratory data analysis to uncover trends, test assumptions, and build descriptive models. MAT LAB provides functions for filtering and smoothing, interpolation, convolution, and fast Fourier transforms (FFTs). Add-on products provide capabilities for curve and surface fitting, multivariate statistics, spectral analysis, image analysis, system identification, and other analysis tasks. Fitting a surface to data with a custom model using MAT LAB and Curve Fitting Toolbox. Enlarge Fitting a surface to data with a custom model using MAT LAB and Curve Fitting Toolbox.

VISUALIZING DATA

MAT LAB provides built-in 2-D and 3-D plotting functions, as well as volume visualization functions. You can use these functions to visualize and understand data and communicate results. Plots can be customized either interactively or programmatically. The MAT LAB plot gallery provides examples of many ways to display data graphically in MAT LAB. For each example, you can view and download source code to use in your MAT LAB application.

Features of MAT LAB

Following are the basic features of MAT LAB –

- It is a high-level language for numerical computation, visualization and application development.
- It also provides an interactive environment for iterative exploration, design and problem solving.
- It provides vast library of mathematical functions for linear algebra, statistics, Fourier analysis, filtering, optimization, numerical integration and solving ordinary differential equations.
- It provides built-in graphics for visualizing data and tools for creating custom plots.
- MAT Lab's programming interface gives development tools for improving code quality maintainability and maximizing performance.
- It provides tools for building applications with custom graphical interfaces.
- It provides functions for integrating MAT LAB based algorithms with external applications and languages such as C, Java, .NET and Microsoft Excel.

Uses of MAT LAB

MAT LAB is widely used as a computational tool in science and engineering encompassing the fields of physics, chemistry, math and all engineering streams. It is used in a range of applications including –

- Signal Processing and Communications
- Image and Video Processing
- Control Systems
- Test and Measurement
- Computational Finance
- Computational Biology

1.1.1 Structures

MAT LAB has structure data types.^[15] Since all variables in MAT LAB are arrays, a more adequate name is "structure array", where each element of the array has the same field names. In addition, MAT LAB supports dynamic field names (field look-ups by name, field manipulations, etc.). Unfortunately, MAT LAB JIT does not support MAT LAB structures, therefore just a simple bundling of various variables into a structure will come at a cost.

1.1.2 Functions

When creating a MAT LAB function, the name of the file should match the name of the first function in the file. Valid function names begin with an alphabetic character, and can contain letters, numbers, or underscores. Functions are also often case sensitive.

1.1.3 Function handles

MAT LAB supports elements of lambda calculus by introducing function handles, or function references, which are implemented either in .m files or anonymous/nested functions.

1.1.4 Classes and object-oriented programming

MAT LAB supports object-oriented programming including classes, inheritance, virtual dispatch, packages, pass-by-value semantics, and pass-by-reference semantics. However, the syntax and calling conventions are significantly different from other languages. MAT LAB has value classes and reference classes, depending on whether the class has *handle* as a super-class (for reference classes) or not (for value classes).

SYSTEM DESIGN

INPUT DESIGN

Input design is a part of overall system design, which requires careful attention. Input of data as designed as user-friendly and easier. Input design is a process of converting the user- oriented description of

the input to the computer based information system into programmer- oriented specification. The objective of the input design is to create an input layout that is easy to follow and prevent operator errors. **Input Data Set:** Collecting dataset from UCI Machine learning repository. the real-life data set, named Wisconsin Breast Cancer is used. The data set is publicly available on UCI machine learning repository and consists of 699 instances with nine continuous attributes. by removing some malignant instances to form a very unbalanced distribution has been employed. The resultant data set had 483 instances (39 (8 percent) malignant and 444 (92 percent) benign instances). The nine continuous attributes are not transformed into categorical attributes.

OUTPUT DESIGN

The output design refers to the results and information that are generated by the system for many end users. Efficient and intelligent output design improves the system relationships with the user and help in decision making. The output of the system is in the form of report. outliers are present among Wisconsin cancer samples, the distribution of gene expression values in cancer samples will have three sets. The Upper set corresponds to activated attributes results while the Lower indicates inactivated attributes result.the Kernel set named Kernel Set, that is a subset of the original data set, which is able to describe the original data set both in terms of data structure and of obtained results Consequently, this outlier issue can be addressed through the idea of detecting a “change point” or “break point” in the ordered gene expression values of the cancer group. A model related to fitting least squares should be effective for this goal A remarkable note should be made for the definition of a new set, called kernel set, that has been demonstrated to be able to generate the “same” output results in terms of rough outlier set with time computational benefits.

FEASIBILITY STUDY

Preliminary investigation examine project feasibility, the likelihood the system will be useful to the organization. The main objective of the feasibility study is to test the Technical, Operational and Economical feasibility for adding new modules and debugging old running system. All system is feasible if they are unlimited resources and infinite time. There are aspects in the feasibility study portion of the preliminary investigation:

- Technical Feasibility
- Operation Feasibility
- Economical Feasibility

TECHNICAL FEASIBILITY

The technical issue usually raised during the feasibility stage of the investigation includes the following:

- Does the necessary technology exist to do what is suggested?
- Do the proposed equipment's have the technical capacity to hold the data required to use the new system?
- Will the proposed system provide adequate response to inquiries, regardless of the number or location of users?
- Can the system be upgraded if developed?
- Are there technical guarantees of accuracy, reliability, ease of access and data security?

Earlier no system existed to cater to the needs of ‘Secure Infrastructure Implementation System’. The current system developed is technically feasible. It is a web based user interface for audit workflow at DB2 Database. Thus it provides an easy access to the users. The database’s purpose is to create, establish and maintain a workflow among various entities in order to facilitate all concerned users in their various capacities or roles. Permission to the users would be granted based on the roles specified.

Therefore, it provides the technical guarantee of accuracy, reliability and security. The software and hard requirements for the development of this project are not many and are already available in-house at NIC or are available as free as open source. The work for the project is done with the current equipment and existing software technology. Necessary bandwidth exists for providing a fast feedback to the users irrespective of the number of users using the system.

OPERATIONAL FEASIBILITY

Proposed projects are beneficial only if they can be turned out into information system. That will meet the organization’s operating requirements. Operational feasibility aspects of the project are to be taken as an

important part of the project implementation. Some of the important issues raised are to test the operational feasibility of a project includes the following: -

- Is there sufficient support for the management from the users?
- Will the system be used and work properly if it is being developed and implemented?
- Will there be any resistance from the user that will undermine the possible application benefits?

This system is targeted to be in accordance with the above-mentioned issues. Beforehand, the management issues and user requirements have been taken into consideration. So there is no question of resistance from the users that can undermine the possible application benefits.

The well-planned design would ensure the optimal utilization of the computer resources and would help in the improvement of performance status.

ECONOMIC FEASIBILITY

A system can be developed technically and that will be used if installed must still be a good investment for the organization. In the economical feasibility, the development cost in creating the system is evaluated against the ultimate benefit derived from the new systems. Financial benefits must equal or exceed the costs. The system is economically feasible. It does not require any addition hardware or software. Since the interface for this system is developed using the existing resources and technologies available at NIC, There is nominal expenditure and economical feasibility for certain.

SYSTEM TESTING AND IMPLEMENTATION

SYSTEM TESTING

System testing is the stage of implementation, which is aimed at ensuring that the system works accurately and efficiently before live operation commences. Testing is vital to the success of the system. System testing makes a logical assumption that if all the parts of the system are correct, the goal will be successfully achieved. The candidate system is subject to a variety of tests. A series of tests are performed for the proposed system before the system is ready for user acceptance testing.

The testing steps are:

- Unit testing
- Integration testing
- Validation testing
- Output testing
- User acceptance testing

UNIT TESTING

Unit testing focuses verification efforts on the smallest unit of software design, the module. This is also known as "module testing". The modules are tested separately. This testing is carried out during programming stage itself. In this testing step, each module is found to be working satisfactorily as regard to the expected output from the module.

INTEGRATION TESTING

Data can be lost across an interface; one module can have an adverse effect on others; sub-functions when combined may not produce the desired major functions; integration testing is a systematic testing for constructing the program structure. While at the same time conducting to uncover errors associated within the interface? The objective is to take unit tested modules and to combine them and test it as a whole. Here correction is difficult because the vast expenses of the entire program complicate the isolation of causes. This is the integration-testing step; all the errors encountered are corrected for the next testing step.

VALIDATION TESTING

Verification testing runs the system in a simulated environment using simulated data. This simulated test is sometimes called alpha testing. This simulated test is primarily looking for errors and monitions regarding end user and decisions design specifications hat where specified in the earlier phases but not fulfilled during construction. Validation refers to the process of using software in a live environment in order to find errors. The feedback from the validation phase generally produces changes in the software to deal with errors and failures that are uncovered. Than a set of user sites is selected that puts the system in to use on a live basis. They are called beta tests.

The beta test suits use the system in day to day activities. They process live transactions and produce normal system output. The system is live in every sense of the word; except that the users are aware they are using a system that can fail. But the transactions that are entered and persons using the system are real. Validation may continue for several months. During the course of validating the system, failure may occur and the software will be changed. Continued use may produce additional failures and need for still more changes.

OUTPUT TESTING

After performing the validation, the next step is output testing of the proposed system, since no system could be useful if it does not produce the required output in the specified format. Asking the users about the format required by them tests the output generated or displayed by the system under consideration. Hence the output format is considered in two ways-one is on screen and another in printed format.

USER ACCEPTANCE TESTING

User acceptance of a system is the key factor for the success of any system. The system under consideration is tested for the user acceptance by constantly keeping in touch with the prospective system users at the time of developing and making changes whenever required. This is done in regard to the following point: An acceptance test has the objective of selling the user on the validity and reliability of the system .it verifies that the system's procedures operate to system specifications and that the integrity of important data is maintained. Performance of an acceptance test is actually the user's show. User motivation is very important for the successful performance of the system. After that a comprehensive test report is prepared. This report shows the system's tolerance, Performance range, error rate and accuracy.

SYSTEM MAINTENANCE

The objectives of this maintenance work are to make sure that the system gets into work all time without any bug. Provision must be for environmental changes which may affect the computer or software system. This is called the maintenance of the system. Nowadays there is the rapid change in the software world. Due to this rapid change, the system should be capable of adapting these changes. In this project the process can be added without affecting other parts of the system. Maintenance plays a vital role. The system is liable to accept any modification after its implementation. This system has been designed to favour all new changes. Doing this will not affect the system's performance or its accuracy. Maintenance is necessary to eliminate errors in the system during its working life and to tune the system to any variations in its working environment. It has been seen that there are always some errors found in the system that must be noted and corrected. It also means the review of the system from time to time.

The review of the system is done for:

- Knowing the full capabilities of the system.
- Knowing the required changes or the additional requirements.
- Studying the performance.

TYPES OF MAINTENANCE:

- Corrective maintenance
- Adaptive maintenance
- Perfective maintenance
- Preventive maintenance

CORRECTIVE MAINTENANCE

Changes made to a system to repair flaws in its design coding or implementation. The design of the software will be changed. The corrective maintenance is applied to correct the errors that occur during that operation time. The user may enter invalid file type while submitting the information in the particular field, then the corrective maintenance will displays the error message to the user in order to rectify the error.

Maintenance is a major income source. Nevertheless, even today many organizations assign maintenance to unsupervised beginners, and less competent programmers. The user's problems are often caused by the individuals who developed the product, not the maintainer. The code itself may be badly written maintenance is despised by many software developers Unless good maintenance service is provided, the client will take

future development business elsewhere. Maintenance is the most important phase of software production, the most difficult and most thankless.

ADAPTIVE MAINTENANCE:

It means changes made to system to evolve its functionalities to change business needs or technologies. If any modification in the modules the software will adopt those modifications. If the user changes the server then the project will adapt those changes. The modification server work as the existing is performed.

PERFECTIVE MAINTENANCE:

Perfective maintenance means made to a system to add new features or improve performance. The perfective maintenance is done to take some perfect measures to maintain the special features. It means enhancing the performance or modifying the programs to respond to the users need or changing needs. This proposed system could be added with additional functionalities easily. In this project, if the user wants to improve the performance further then this software can be easily upgraded.

PREVENTIVE MAINTENANCE:

Preventive maintenance involves changes made to a system to reduce the changes of features system failure. The possible occurrence of error that might occur are forecasted and prevented with suitable preventive problems. If the user wants to improve the performance of any process then the new features can be added to the system for this project.

CHAPTER 4

EXPERIMENTAL SETUP AND PROCEDURE

We present the experimental results from the segmentation of three types of fluorescent cellular images: synthetic cell images, nuclei images with ground truth, and brain cell microscopic images. The first two types of image data are used to evaluate the quantitative Performance of the four segmentation methods and to compare the results to the ground truth. The brain cell images are segmented with qualitative performance analysis due to the lack of ground truth.

QUANTITATIVE MEASURE

We use the traditional precision, recall, and F-score as the quantitative measures in pixel level. These measures are standard techniques used to evaluate the quality of the segmentation results against the ground truth.

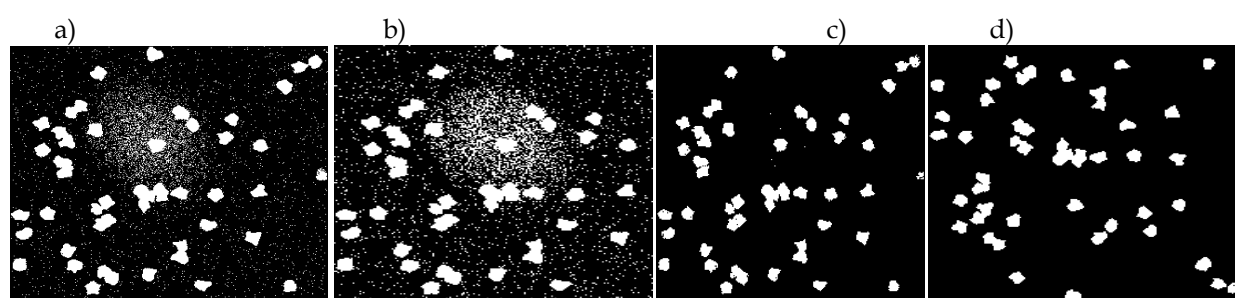


Fig. (2). Segmentation result for synthetic cell images of low quality in Fig. (1a). a) K-means result, b) EM result, c) Otsu's result, d) GMAC result.

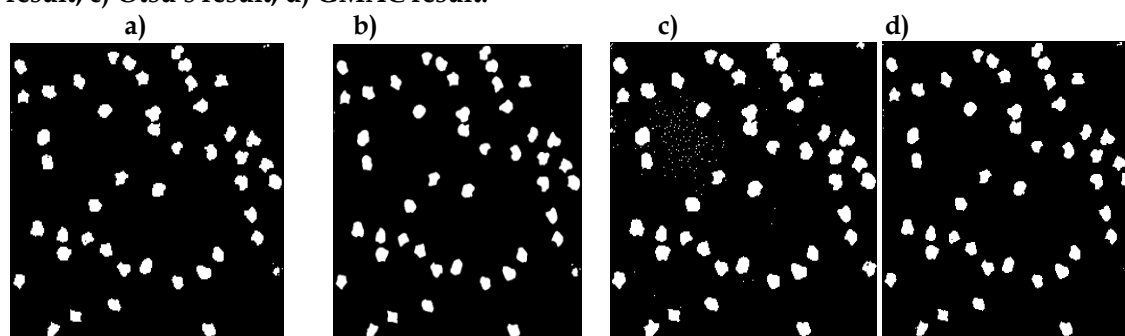


Figure (3). Segmentation result for synthetic cell image of high

quality in Fig. (1b). a) K-means result, b) EM result, c) Otsu’s result, d) GMAC result

measures quantify discrepancy between segmentation results and binary ground truth mask as follows

$$\text{precision} = \frac{\#SR \cap GT}{\#SR} \rightarrow (26)$$

$$\text{recall} = \frac{\#(SR \cap GT)}{\#GT} \rightarrow (27)$$

$$\text{f-score} = \frac{2 \cdot (\text{precision} \cdot \text{recall})}{\text{precision} + \text{recall}} \rightarrow (28)$$

where SR is the segmentation result and GT is the ground truth of images. The symbol ‘#’ refers to the pixel numbers in the sets. LL

SEGMENTATION OF SYNTHETIC DATA

We select the second benchmark set which consists of multichannel cell images because we do not have suitable real cell images with ground truth for evaluation. In this set, nuclei, cytoplasm, and sub cellular components have been simulated by tuning parameters such as size, location, randomness of shape, and other background or fluorescence parameters. The image sets are divided into two subsets: high quality and low quality (examples shown in Fig. 1), each consisting of 20 cell images. The second set has overlapping cells and a noisy background. Each image contains 50 cells. As each simulated image has a corresponding binary mask as ground truth, binary operations can easily calculate the quantitative measure defined above.

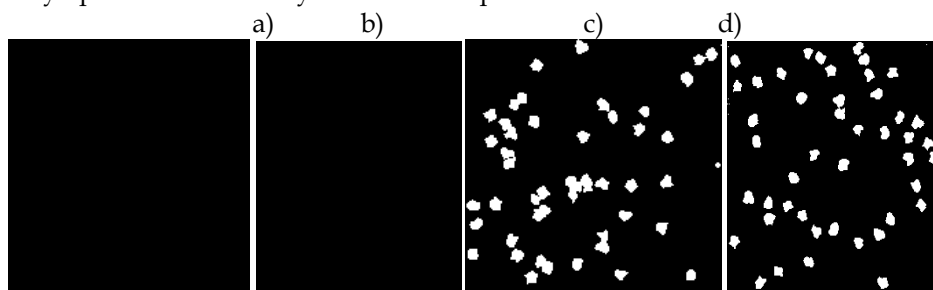
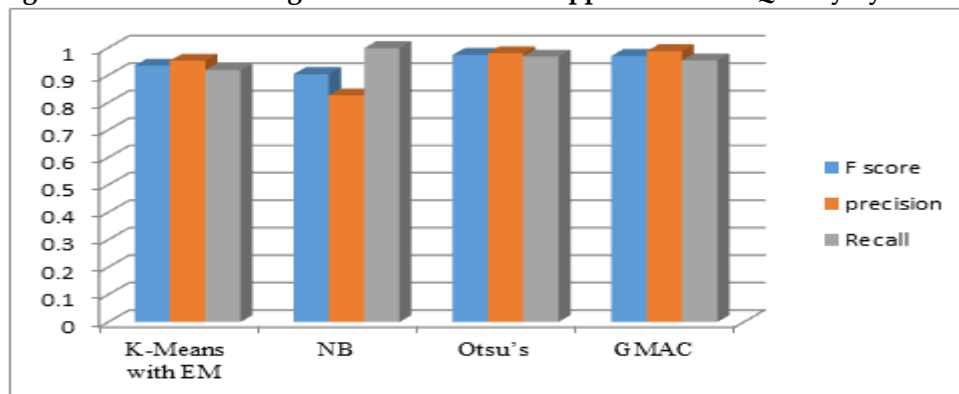


Fig. (1). Synthetic cell images a) (low quality) with noisy background and overlapping cells, b) (high quality) without noise

values for the segmentation results using sub cellular images with high quality. We observe that the segmentation results of lower quality images, with noisier backgrounds and overlapping cells, have worse results than those in high quality images. Kmeans, Otsu’s threshold and GMAC obtain similar segmentation quality in both sets of images, measured by Fscore, precision, and recall. Their performance is more robust against noises than EM. Moreover, the EM algorithm has lower precision, while keeping much higher recall values, especially for cell images with noisy backgrounds.

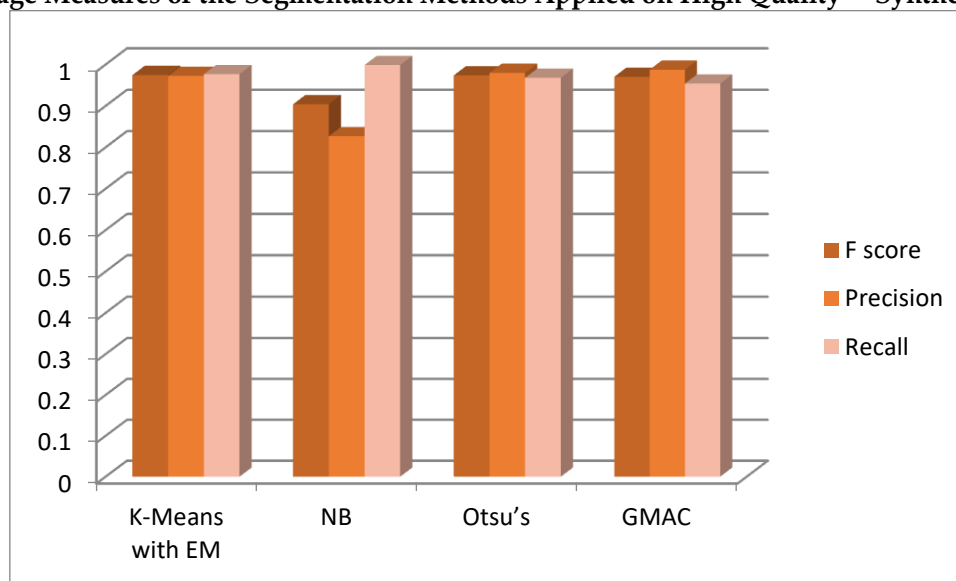
| | F score | precision | Recall |
|-----------------|---------|-----------|--------|
| K-Means with EM | 0.9350 | 0.9530 | 0.9180 |
| NB | 0.9040 | 0.8267 | 0.9986 |
| Otsu’s | 0.9738 | 0.9798 | 0.9679 |
| GMAC | 0.9703 | 0.9874 | 0.9538 |

Table 1. Average Measures of the Segmentation Methods Applied on Low Quality Synthetic Cell Images.



| | F score | Precision | Recall |
|-----------------|---------|-----------|--------|
| K-Means with EM | 0.9745 | 0.9726 | 0.9765 |
| NB | 0.9040 | 0.8267 | 0.9986 |
| Otsu's | 0.9738 | 0.9798 | 0.9679 |
| GMAC | 0.9703 | 0.9874 | 0.9538 |

Table 2. Average Measures of the Segmentation Methods Applied on High Quality Synthetic Cell Images.



RESULTS AND DISCUSSION

The future work will make further modifications to the existing deep learning algorithm, which include slight optimization to the network architecture, and optimization of the loss function. Second, we will explore new network architectures that will result in better predictions and will reduce the risk of post-processing errors. Third, we will investigate and test additional data augmentation strategies, which include generating synthetic data. Fourth, we will work on improving the speed and accuracy of the post-processing algorithm. Furthermore, a possible improvement to our algorithm will be to predict the locations of cell boundaries using the SVM AND KNN model, and therefore to eliminate or, at least, to reduce the number of post-processing steps.

In one of our early experiments, we tried to define a cell boundary class using the cell-to-cell borders in the ground truth segmentation. Unfortunately, that resulted with poor prediction of the cell boundaries. That poor performance could be attributed to the imperfect nature of our ground truth segmentation results. In future work, we may investigate adding higher weights in the loss function on pixels close to the cell boundaries.

CONCLUSION

A novel K-Means with EM method for cell segmentation in fluorescence microscopy images was developed. Satisfactory results were generated with this approach. This method is suitable for cell separation, which allows appropriate cell-by-cell characterization for complex studies, such as virus infection analysis. First, a Machine learning algorithm was used to extract the cells from the background. This initial segmented image was the input for the two-stage algorithm of the Machine learning method. It applies the Split and Merge processes based on the Machine learning transform to separate the cells correctly. The split process identifies the clustered cells using fitted features of the cells like area and solidity, and then the distance

transform is calculated to apply Machine learning. The merge process uses the area and eccentricity to identify the over-segmented regions and employs morphological operations to eliminate the divisions.

Furthermore, this method follows the irregular shape of the cells since it is not based on a geometric adjustment. Compared with the state-of-the-art methodologies as deep learning architectures, they outperformed our method, but K-Means(KNN), SVM and J48 with EM Machine learning does not require a training process, which is suitable for databases with reduced data. Even though the K-Means with EM Machine learning cell segmentation method performed well in identifying cells in a fluorescence image, additional research is needed to improve the indicators for missing cells and the added noise.

REFERENCES

- [1] C. Li, H. Chen, X. Li, N. Xu, Z. Hu, D. Xue, S. Qi, H. Ma, L. Zhang, and H. Sun, "A review for prostate histopathology image analysis using machine vision approaches," *Artif. Intell. Rev.*, pp. 1-42, Feb. 2020, doi:10.1007/s10462-020-09808-7.
- [2] M. Rahaman, C. Li, X. Wu, Y. Yao, Z. Hu, T. Jiang, X. Li, and S. Qi, "A survey for prostate cytopathology image analysis using deep learning," *IEEE Access*, vol. 8, no. 1, pp. 61687-61710, 2020.
- [3] C. Li, D. Xue, X. Zhou, J. Zhang, H. Zhang, Y. Yao, F. Kong, L. Zhang, and H. Sun, "Transfer learning based classification of prostate cancer immunohistochemistry images," in *Proc. 3rd Int. Symp. Image Comput. Digit. Med. (ISICDM)*, 2019, pp. 102-106.
- [4] C. Li, H. Chen, L. Zhang, N. Xu, D. Xue, Z. Hu, H. Ma, and H. Sun, "Prostate histopathology image classification using multilayer hidden conditional random fields and weakly supervised learning," *IEEE Access*, vol. 7, pp. 90378-90397, 2019.
- [5] B. Zhang, S. Qi, P. Monkam, C. Li, F. Yang, Y.-D. Yao, and W. Qian, "Ensemble learners of multiple deep CNNs for pulmonary nodules classification using CT images," *IEEE Access*, vol. 7, pp. 110358-110371, 2019.
- [6] Gautam, H. K. K., N. Jith, A. K. Sao, A. Bhavsar, and A. Natarajan, "Considerations for a PAP smear image analysis system with CNN features," 2019, *arXiv:1806.09025*. [Online]. Available: <http://arxiv.org/abs/1806.09025>
- [7] N. Crossley, C. Tipton, T. Meier, M. Sudhoff, and J. Kharofa, "The value of hybrid interstitial tandem and ring applicators for organ at risk dose reduction in small volume prostate cancer," *Brachytherapy*, vol. 17, no. 4, p. S111, Jul. 2019.
- [8] C. Qian, Y. Yu, and Z.-H. Zhou, "Analyzing evolutionary optimization in noisy environments," *Evol. Comput.*, vol. 26, no. 1, pp. 1-41, Mar. 2020.
- [9] A. Jothi and V. M. A. Rajam, "A survey on automated cancer diagnosis from histopathology images," *Artif. Intell. Rev.*, vol. 48, no. 1, pp. 31-81, Jun. 2019.
- [10] H. Komagata, T. Ichimura, Y. Matsuta, M. Ishikawa, K. Shinoda, N. Kobayashi, and A. Sasaki, "Feature analysis of cell nuclear chromatin distribution in support of prostate cytology," *J. Med. Imag.*, vol. 4, no. 4, p. 1, Oct. 2020.
- [11] L. Wei, Q. Gan, and T. Ji, "Prostate cancer histology image identification method based on texture and lesion area features," *Comput. Assist. Surg.*, vol. 22, no. 1, pp. 186-199, Oct. 2019.
- [12] M. M. Ghazi, B. Yanikoglu, and E. Aptoula, "Plant identification using deep neural networks via optimization of transfer learning parameters," *Neurocomputing*, vol. 235, pp. 228-235, Apr. 2020.
- [13] F. Shoeleh and M. Asadpour, "Graph based skill acquisition and transfer learning for continuous reinforcement learning domains," *Pattern Recognit. Lett.*, vol. 87, pp. 104-116, Feb. 2021.
- [14] E. Gocer, B. Goksel, J. B. Elder, V. K. Puduvali, J. J. Otero, and M. N. Gurcan, "Quantitative validation of anti-PTBP1 antibody for diagnostic neuropathology use: Image analysis approach," *Int. J. Numer. Methods Biomed. Eng.*, vol. 33, no. 11, p. e2862, Nov. 2020.
- [15] B. Taha, J. Dias, and N. Werghe, "Classification of prostate-cancer using pap-smear images: A convolutional neural network approach," in *Proc. Annu. Conf. Med. Image Understand. Anal. Berlin, Germany: Springer*, 2019, pp. 261-272.
- [16] L. Zhang, L. Lu, I. Nogueira, R. M. Summers, S. Liu, and J. Yao, "DeepPap: Deep convolutional networks for prostate cell classification," *IEEE J. Biomed. Health Inform.*, vol. 21, no. 6, pp. 1633-1643, Nov. 2019.
- [17] L. Nanni, S. Ghidoni, and S. Brahmam, "Handcrafted vs. Non-handcrafted features for computer vision classification," *Pattern Recognit.*, vol. 71, pp. 158-172, Nov. 2019.
- [18] Chanthathi, Sasibhushan Rao. (2021). How the Power of Machine - Machine Learning, Data Science and NLP Can Be Used to Prevent Spoofing and Reduce Financial Risks. 10.13140/RG.2.2.18761.76640.
- [19] J. Su, X. Xu, Y. He, and J. Song, "Automatic detection of prostate cancer cells by a two-level cascade classification system," *Anal. Cellular Pathol.*, vol. 2016, no. 4, 2020, Art. no. 9535027.
- [20] M. A. Devi, S. Ravi, J. Vaishnavi, and S. Punitha, "Classification of prostate cancer using artificial neural networks," *Procedia Comput. Sci.*, vol. 89, pp. 465-472, 2020.
- [21] F. Chollet, "Xception: Deep learning with depthwise separable convolutions," 2019, arXiv:1610.02357. [Online]. Available: <http://arxiv.org/abs/1610.02357>.
- [22] Naga Ramesh Palakurti, 2023. "Evolving Drug Discovery: Artificial Intelligence and Machine Learning's Impact in Pharmaceutical Research" *ESP Journal of Engineering & Technology Advancements* 3(3): 136-147. [[Link](#)]

- [23] Naga Ramesh Palakurti, 2022. "AI Applications in Food Safety and Quality Control" ESP Journal of Engineering & Technology Advancements 2(3): 48-61. [Link]
- [24] Chanthati, S. R. (2024). An automated process in building organic branding opportunity, budget Intensity, recommendation in seasons with Google trends data. Sasibhushan Rao Chanthati. <https://doi.org/10.30574/wjaets.2024.12.2.0326>
- [25] Kumar Shukla, Nimeshkumar Patel, Hirenkumar Mistry, 2024." Securing The Cloud: Strategies and Innovations In Network Security For Modern Computing Environments" Volume 11, Issue 04 pp. 1786-1796. [Link]
- [26] Muthukumaran Vaithianathan, Mahesh Patil, Shunye Frank Ng, Shiv Udkar, 2024. "Verification of Low-Power Semiconductor Designs Using UVM", ESP Journal of Engineering & Technology Advancements 4(3): 28-44.
- [27] Doctor, A., B. Vondenbusch, and J. Kozak. "Bone segmentation applying rigid bone position and triple shadow check method based on RF data." Acta of Bioengineering and Biomechanics, 13.2 (2011): 3-11.
- [28] Jaseem Pookandy, Enhancing Customer Relationship Management with Salesforce: A Comprehensive Review, International Journal of Computer Engineering and Technology (IJCET), 15(4), 2024, pp. 64-84
- [29] Muthukumaran Vaithianathan, Mahesh Patil, Shunye Frank Ng, Shiv Udkar, 2024. "Energy-Efficient FPGA Design for Wearable and Implantable Devices" ESP International Journal of Advancements in Science & Technology (ESP-IJAST) Volume 2, Issue 2: 37-51.
- [30] Jacopo Pianigiani, Michal Styszynski, Atul S Moghe, Joseph Williams, Sahana Sekhar Palagrahara Chandrashekar, Tong Jiang, Rishabh Ramakant Tulsian, Manish Krishnan, Soumil Ramesh Kulkarni, Vinod Nair, Jeba Paulaiyan, Sukhdev S. Kapur, Ashok Ganesan, 2020. Automation of Maintenance Mode Operations for Network Devices, US10742501B1. [Link]
- [31] Chandrakanth Lekkala, "Utilizing Cloud - Based Data Warehouses for Advanced Analytics: A Comparative Study", International Journal of Science and Research (IJSR), Volume 11 Issue 1, January 2022, pp. 1639-1643, <https://www.ijsr.net/getabstract.php?paperid=SR24628182046>
- [32] Julian, Anitha, Mary, Gerardine Immaculate, Selvi, S., Rele, Mayur & Vaithianathan, Muthukumaran (2024) Blockchain based solutions for privacy-preserving authentication and authorization in networks, Journal of Discrete Mathematical Sciences and Cryptography, 27:2-B, 797-808, DOI: [10.47974/JDMSC-1956](https://doi.org/10.47974/JDMSC-1956)
- [33] Muthukumaran Vaithianathan, 2024. "Digital Signal Processing for Noise Suppression in Voice Signals", IJCSPUB - INTERNATIONAL JOURNAL OF CURRENT SCIENCE (www.IJCSPUB.org), ISSN: 2250-1770, Vol.14, Issue 2, page no.72-80, April-2024, Available: <https://rjpn.org/IJCSPUB/papers/IJCSP24B1010.pdf>
- [34] Muthukumaran Vaithianathan, "Real-Time Object Detection and Recognition in FPGA-Based Autonomous Driving Systems," International Journal of Computer Trends and Technology, vol. 72, no. 4, pp. 145-152, 2024. Crossref, <https://doi.org/10.14445/22312803/IJCTT-V72I4P119>
- [35] Muthukumaran Vaithianathan, Mahesh Patil, Shunye Frank Ng, Shiv Udkar, 2023. "Comparative Study of FPGA and GPU for High-Performance Computing and AI" ESP International Journal of Advancements in Computational Technology (ESP-IJACT) Volume 1, Issue 1: 37-46. [PDF]
- [36] Muthukumaran Vaithianathan, Mahesh Patil, Shunye Frank Ng, Shiv Udkar, 2024. "Low-Power FPGA Design Techniques for Next-Generation Mobile Devices" ESP International Journal of Advancements in Computational Technology (ESP-IJACT) Volume 2, Issue 2: 82-93. [PDF]
- [37] Dhamotharan Seenivasan, Muthukumaran Vaithianathan, 2023. "Real-Time Adaptation: Change Data Capture in Modern Computer Architecture" ESP International Journal of Advancements in Computational Technology (ESP-IJACT) Volume 1, Issue 2: 49-61. [PDF]
- [38] Muthukumaran Vaithianathan, Mahesh Patil, Shunye Frank Ng, Shiv Udkar, 2024. "Integrating AI and Machine Learning with UVM in Semiconductor Design" ESP International Journal of Advancements in Computational Technology (ESP-IJACT) Volume 2, Issue 3: 37-51. [PDF]
- [39] Chanthati, Sasibhushan Rao. (2021). A segmented approach to encouragement of entrepreneurship using data science. World Journal of Advanced Engineering Technology and Sciences. <https://doi.org/10.30574/wjaets.2024.12.2.0330>, [link]
- [40] Patel, N. (2024, March). SECURE ACCESS SERVICE EDGE(SASE): "EVALUATING THE IMPACT OF CONVERGED NETWORK SECURITY ARCHITECTURES IN CLOUD COMPUTING." Journal of Emerging Technologies and Innovative Research. <https://www.jetir.org/papers/JETIR2403481.pdf>
- [41] Vishwanath Gojanur, Aparna Bhat, "Wireless Personal Health Monitoring System", IJETCAS: International Journal of Emerging Technologies in Computational and Applied Sciences, eISSN: 2279-0055, pISSN: 2279-0047, 2014. [Link]
- [42] Mistry, H., Shukla, K., & Patel, N. (2024). Transforming Incident Responses, Automating Security Measures, and Revolutionizing Defence Strategies through AI-Powered Cybersecurity. Journal of Emerging Technologies and Innovative Research, 11(3), 25. <https://www.jetir.org/>
- [43] Aparna Bhat, "Comparison of Clustering Algorithms and Clustering Protocols in Heterogeneous Wireless Sensor Networks: A Survey," 2014 INTERNATIONAL JOURNAL OF SCIENTIFIC PROGRESS AND RESEARCH (IJSR)-ISSN : 2349-4689 Volume 04- NO.1, 2014. [Link]
- [44] Shashikant Tank Kumar Mahendrabhai Shukla, Nimeshkumar Patel, Veeral Patel, 2024." AI BASED CYBER SECURITY DATA ANALYTIC DEVICE", 414425-001, [Link]

- [45] Aparna Bhat, Rajeshwari Hegde, "Comprehensive Study of Renewable Energy Resources and Present Scenario in India," 2015 IEEE International Conference on Engineering and Technology (ICETECH), Coimbatore, TN, India, 2015. [Link]
- [46] Sarangkumar Radadia Kumar Mahendrabhai Shukla ,Nimeshkumar Patel ,Hirenkumar Mistry,Keyur Dodiya 2024." CYBER SECURITY DETECTING AND ALERTING DEVICE", 412409-001, [Link]
- [47] Aparna K Bhat, Rajeshwari Hegde, 2014. "Comprehensive Analysis Of Acoustic Echo Cancellation Algorithms On DSP Processor", International Journal of Advance Computational Engineering and Networking (IJACEN), volume 2, Issue 9, pp.6-11. [Link]
- [48] Nimeshkumar Patel, 2022." QUANTUM CRYPTOGRAPHY IN HEALTHCARE INFORMATION SYSTEMS: ENHANCING SECURITY IN MEDICAL DATA STORAGE AND COMMUNICATION", Journal of Emerging Technologies and Innovative Research, volume 9, issue 8, pp.g193-g202. [Link]
- [49] Bhat, A., & Gojanur, V. (2015). Evolution Of 4g: A Study. International Journal of Innovative Research in ComputerScience & Engineering (IJIRCSE). Booth, K. (2020, December 4). How 5G is breaking new ground in the construction industry. BDC Magazine.<https://bdcmagazine.com/2020/12/how-5g-is-breaking-new-ground-in-the-constructionindustry/>. [Link]
- [50] Nimeshkumar Patel, 2021." SUSTAINABLE SMART CITIES: LEVERAGING IOT AND DATA ANALYTICS FOR ENERGY EFFICIENCY AND URBAN DEVELOPMENT", Journal of Emerging Technologies and Innovative Research, volume 8, Issue 3, pp.313-319. [Link]
- [51] Bhat, A., Gojanur, V., & Hegde, R. (2014). 5G evolution and need: A study. In International conference on electrical, electronics, signals, communication and optimization (EESCO) – 2015.[Link]
- [52] A. Bhat, V. Gojanur, and R. Hegde. 2015. 4G protocol and architecture for BYOD over Cloud Computing. In Communications and Signal Processing (ICCSP), 2015 International Conference on. 0308-0313. Google Scholar. [Link]
- [53] M. Hindka, "Securing the Digital Backbone: An In-depth Insights into API Security Patterns and Practices", Computer Science and Engineering, Vol. 14, No. 2, pp. 35-41, 2024.
- [54] M. Hindka, "Design and Analysis of Cyber Security Capability Maturity Model", International Research Journal of Modernization in Engineering Technology and Science, Vol. 6, No. 3, pp. 1706-1710, 2024.
- [55] Hindka, M. (2024, June). Optimization Accuracy of Secured Cloud Systems Using Deep Learning Model. In 2023 4th International Conference on Intelligent Technologies (CONIT) (pp. 1-5). IEEE.